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(54) Title: POLYPEPTIDES DERIVED FROM RETINOIC ACID-RELATED ORPHAN RECEPTOR (ROR), AND THEIR APPLICATIONS

(57) Abstract: The invention relates to polypeptides derived from the retinoic acid-related orphan receptor (ROR) in mammals, characterized in that they are delimited in their N-terminal extremity by an amino-acid located between positions 1 to 209, and in their C-terminal extremity by an amino-acid located between positions 450 to 452 of the rat RORß, α, or γ, or by an amino-acid located at corresponding positions in nuclear receptor ROR of other subtypes than α, β and γ, and/or of the other mammals. The invention also relates to the use of these polypeptides, or of the molecular complexes or the crystals containing them, for carrying out: -a process for the screening of a ROR-LBD ligand which is an agonist, or an antagonist of said receptor, - or a process for the analysis of the tridimensional structure of the complexes formed with said polypeptides, molecular complexes or crystals and a particular compound.

POLYPEPTIDES DERIVED FROM RETINOIC ACID-RELATED ORPHAN RECEPTOR (ROR), AND THEIR APPLICATIONS

Field of Invention

An aspect of this invention is to obtain crystal structure from orphan receptors by using a heterologous expression system, which will not only produce high amount of the desired protein but may also furnish a pseudo-ligand. The presence of this fortuitous molecule is important to stabilize an active agonist conformation by adding concomitantly a co-activator peptide. These two elements avoid any other non-active alternative conformations.

This method is illustrated by crystals of brain specific retinoic acid-related orphan receptor ligand binding domain (RORβ-LBD) in complex with a co-activator peptide and a fortuitous fatty acid ligand. This invention also relates to methods of using DNA sequence or derived constructions to produce proteins in order either to find out the physiological ligand or to screen for synthetic analogues. This invention also relates to methods for designing and selecting ligands that bind to the RORβ and methods of using such ligands. It refers also to the use of DNA sequences of RORβ or derived sequences thereof in order to identify other proteins which interact with RORβ. Obviously the object of this invention is also the usage of the structure of similar or homologous proteins or protein complexes, particularly all these claims are applied to the two isotypes RORα and γ.

Background of this Invention

The orphan retinoic acid-related orphan receptor β (RORβ), also called retinoid Z receptor β (RZRβ) (NR1F2) belongs to the nuclear receptor (NR) superfamily and is expressed in areas of the central nervous system. The ligand-dependent activity of the nuclear receptor makes them obvious targets for drug design in many therapeutic areas. However in the case of orphan receptors, the ligand is not known and even the existence of a ligand is not proven. RORβ was never shown to bind retinoic acid. RORβ regulates genes whose products play a role in the context of sensory input integration as well as in the context of the biological clock. A behavioral phenotype of RORß -/- mice was observed and seems to be similar to the phenotype described > 40 years ago for a spontaneous mouse mutation called *vacillans* (Sirlin, 1956). These mice display a duck-like gait, transient male incapability to sexually reproduce and a severely disorganised retina that suffer from post-natal degeneration.

Two other closely nuclear receptors are RORα and RORγ. RORα presents 61% identity and 74% similarity with RORβ. RORα is rather ubiquitously expressed (Becker-André et al., 1993) and has been demonstrated to play important roles in cerebellum development and immune response (Matysiak-Scholze and Nehls, 1997; Koibuchi and Chin., 1998). *Staggerer* mice were found to carry a deletion within the RORα gene that prevents translation of the ligand-binding domain. They present a severe cerebellar ataxia related to a defect in developpement of Purkinje cells. Certain functions of the immune system are also affected (Hamilton & al., 1996).

Certain functions of the immune system are also affected (Hamilton & al., 1996). RORα is also constitutively expressed during myogenesis (Lau et al. , 1999).

The expression of RORγ is found mainly in skeletal muscle (Hirose et al., 1994) and is induced in the middle stage of adipocyte differentiation (Kurebayashi S., and Hirose T, 1998).

As with the other members of the nuclear receptor family, RORβ has several functional domains including a DNA binding domain (DBD), and a 250 residue ligand-binding domain (LBD) which contains the ligand -binding site, and is responsible for switching on the ligand-binding function.

It would be advantageous to devise methods and compositions for reducing the time required to discover ligands to the RORβ, synthesize such compounds and administer such compounds to organisms to modulate physiological processes regulated by the RORβ receptor or any of its isotypes α or β.

There have been no crystals reported so far of any orphan receptor in the agonist bound conformation. The structure of USP, the insect ortholog of RXR, has been published recently. Though RXRs bind 9c-RA, USP fail to bind this ligand and must still be considered as an orphan receptor. Juvenile hormones have been proposed to be the natural ligands of USP but matter is still controversial. Nevertheless, the USP LBD structure is in an antagonist-like conformation. We report discovered the first crystal structure of the orphan receptor ligand-binding domain (RORβ-LBD) in the agonist bound conformation, which represents the transcriptionally active form of nuclear receptor.

Summary of the Invention

The invention relates to polypeptides derived from the retinoic acid-related orphan receptor (ROR) in mammals, characterized in that they comprise at least the amino-acid sequence delimited in its N-terminal extremity by the first amino acid of the H1 helix, and in its C-terminal extremity by the last amino acid of the H12 helix.

The invention relates more particularly to polypeptides derived from the retinoic acid-related orphan receptor (ROR) in mammals, characterized in that they are delimited in their N-terminal extremity by an amino-acid located between positions 1 to 209 of the rat, human, or murine RORβ, α, or γ, as represented on figure 3, or by an amino-acid located at corresponding positions in nuclear receptor ROR of other subtypes than α, β and γ, and/or of other mammals, and in their C-terminal extremity by an amino-acid located between positions 450 to 452 of the rat, human, or murine RORβ, α, or γ, as represented on figure 3, or by an amino-acid located at corresponding positions in nuclear receptor ROR of other subtypes than α, β and γ, and/or of other mammals.

The invention relates more particularly to polypeptides derived from the retinoic acid-related orphan receptor (ROR) in mammals, characterized in that they are delimited in their N-terminal extremity by an amino-acid located between positions 1 to 209 of the human or rat nuclear receptor RORβ, as represented on figure 3, or by an amino-acid located at corresponding positions in nuclear receptor ROR of other subtypes, such as RORα, and RORγ, as represented on figure 3, and/or of other mammals, and in their C-terminal extremity by an amino-acid located between positions 450 to 452 of the human or rat nuclear receptor RORβ, as represented on figure 3, or by an amino-acid located at corresponding positions in nuclear receptor ROR of other subtypes, such as RORα, and RORγ, and/or of other mammals.

The invention also concerns polypeptides derived from the retinoic acid-related orphan receptor (ROR) in mammals, characterized in that they are delimited in their N-terminal extremity by the methionine in position 209 of the human or rat nuclear receptor RORβ, as represented on figure 3, or by the methionine or another amino-acid such as leucine located at a corresponding position in nuclear receptor ROR of other subtypes, such as RORα, and RORγ, and/or of other mammals, and in its C-terminal extremity by the phenylalanine in position 450 of the human or rat nuclear receptor RORβ, as represented on figure 3, or by the phenylalanine or another amino-acid located at a corresponding position in nuclear receptor ROR of other subtypes, such as RORα, and RORγ, and/or of other mammals.

Advantageously, polypeptides as defined above according to the invention, are characterized in that at least the approximately 100 to 200 first amino-acids of the N-terminal part of the sequence of said receptor is deleted.

Polypeptides according to the invention defined above are more particularly characterized, in that they are polypeptides derived from the nuclear receptor ROR, wherein the binding properties of the ligand-binding domain, or LBD, of said receptor, are maintained.

The invention relates more particularly to polypeptides derived from the nuclear receptor RORβ, of mammals, such as human or rat, these derived polypeptides comprising a polypeptide as defined above, such as the polypeptides delimited by the amino-acids located in positions 201 to 459 of the sequences of rat or human RORβ represented on figure 3, said polypeptides being characterized in that at least one of the cysteine in position 454 or in position 458 of the amino-acid sequence of said nuclear

receptor RORβ, as represented on figure 3, is deleted or substituted by another amino-acid, natural or not, such as alanine or serine.

The invention relates more particularly to polypeptides as defined above, characterized in that :

- the N-terminal sequence delimited by the amino-acids in position 1 to 200 of the receptor, is deleted,
- and the C-terminal sequence starting from the amino-acid in position 450 of the human or rat nuclear receptor RORβ represented on figure 3, or from the amino-acid located at a corresponding position in nuclear receptor ROR of other subtypes, such as RORα, and RORγ, as represented on figure 3, and/or of other mammals, and more preferably from the amino-acid in position 451, 452, or 453, is deleted.

The invention relates more particularly to polypeptides as defined above, characterized in that they correspond to the fragments of mammals ROR, and more particularly of rat, human, or murine RORβ, α, or γ, delimited in their N-terminal extremity by the amino acid located in one of the positions 201 to 209 of the ROR sequences represented on figure 3, and in their C-terminal extremity by the amino acid located in one of the positions 451 or 452, of the ROR sequences represented on figure 3.

The invention concerns more particularly polypeptides as defined above, chosen among :

- the fragment delimited by the amino acids located in positions 209 to 452 of :
  . the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 2,
  . the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 3,
  . the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 4,
  . the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 5,
  . the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 6,
  . the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 7,
- the fragment delimited by the amino acids located in positions 208 to 452 of :
  . the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 8,
  . the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 9,
  . the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 10,
  . the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 11,
  . the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 12,
  . the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 13,
- the fragment delimited by the amino acids located in positions 208 to 451 of :
  . the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 14,
  . the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 15,
  . the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 16,
  . the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 17,
  . the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 18,

. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 19,
- the fragment delimited by the amino acids located in positions 209 to 451 of :
. the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 20,
. the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 21,
. the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 22,
. the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 23,
. the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 24,
. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 25,
- the fragment delimited by the amino acids located in positions 201 to 451 of :
. the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 26,
. the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 27,
. the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 28,
. the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 29,
. the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 30,
. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 31,
- the fragment delimited by the amino acids located in positions 201 to 452 of :
. the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 32,
. the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 33,
. the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 34,
. the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 35,
. the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 36,
. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 37.

Polypeptides as defined above according to the invention, are more particularly characterized by the following characteristics :
- they have the properties of binding a ligand and of transactivation of the LBD of the receptor ROR,
- they are soluble in aqueous solvants,
- they are crystallisable in aqueous solvents, especially by the hanging drop vapour diffusion method, more particularly at approximately 4°C,

or polypeptides or peptide sequences derived of those above mentioned, for example by suppression, addition or substitution of one or several amino acids, these polypeptides or peptide sequences having the characterisitics above mentioned.

The invention also concerns molecular complexes comprising a polypeptide as defined above, said polypeptide being in association with :
- a ROR-LBD ligand which is an agonist, such as stearic acid, or an antagonist of the ROR-LBD, such as retinoic acid,
- and/or with a co-peptide having a sequence of approximately 15-20 amino-acids and comprising the co-activator motif LXXLL or a co-repressor motif (I/L)XX(V/I)I or

LXX(H/I)IXXX(I/L) wherein X represents any amino acid, natural or not, such as co-peptides chosen among fragments of co-activators of transcription, especially those of the p160 family, and more particularly among fragments of the co-activators SRC1, such as the fragment 686-700 of SRC1, or among fragments of co-repressors of transcription.

The invention also relates to nucleotide sequence coding for a polypeptide as defined above.

The invention also relates to nucleotide sequence as defined above, associated to elements necessary for the transcription of this sequence, particularly a promoter and a terminator of transcription.

The invention also concerns vector, particularly plasmid, comprising a nucleotide sequence as defined above.

The invention also relates to host cells, such as *E.coli*, transformed with a vector as defined above.

The invention also relates to a process for obtaining a polypeptide, or a molecular complex, as defined above, characterized in that it comprises :

- a step of transforming host cells with a nucleotide sequence as defined above, using a vector as defined above,
- a step of cultivating the transformed host cell as defined above thus obtained, in an appropriate culture medium,
- and the recovery, and if necessary, the purification of the recombinant polypeptide or molecular complex obtained.

The invention also relates to a crystal comprising a polypeptide according, or a molecular complex, as defined above.

Advantageously, a crystal as defined above, is characterized in that it diffracts to at least 3 angstrom resolution and has a crystal stability within 5% of its unit cell dimensions.

Preferred crystal as defined above, is such that the ROR-LBD has the following unit cell dimensions in angstroms : a= 52.302 Å, b= 58.490 Å and c= 106.036 Å, $\alpha=\beta=\chi=90$ °, and an orthorhombic space group P212121.

The invention also relates to a crystal as defined above, such as obtained by carrying out a process mentioned above, and comprising a step of crystallisation in aqueous solvents of the polypeptides, or the molecular complexes, as defined above, especially at 4°C by the hanging drop vapour diffusion method.

The invention also relates to the use of the polypeptides, or of the molecular complexes, or of the crystals, as defined above, for carrying out:

- a process for the screening of a ROR-LBD ligand which is an agonist, or an antagonist of said receptor, or for the screening of ligands that perturb the structure of the receptor and having an effect on the recruitment of cofactors (co-activators and co-repressors) and hence on gene regulation,
- or a process for the analysis of the tridimensional structure of the complexes formed with said polypeptides, molecular complexes or crystals and a particular compound.

The invention relates more particularly to the use mentioned above, for the screening of compounds acting as agonists or antagonists of ROR, said compounds being useful in the frame of the treatment of pathologies related to the central nervous system, the retinal organisation, the sensorial signal integration, the motricity, and sterility.

The invention also relates to a process for the screening of a ROR-LBD ligand which is an agonist, or an antagonist of said receptor, said process comprising the following steps :

- contacting a polypeptide, or a molecular complex, or a crystal according, as defined above, advantageously linked to a solid support, with the particular compound susceptible to be a ROR-LBD ligand, preferably one of the said polypeptide, or molecular complex, or crystal, or tested ligand, being labelled, such as with a fluorescent, radioactive or enzymatic label,
- detection of the possible association between the said polypeptide, or molecular complex, or crystal, and the tested ligand, by measuring the used label, especially after

rinsing the support used in the preceding step, or by mass spectrometry under non denaturing conditions.

The invention also relates to a process for the analysis of the tridimensional structure of the complexes formed with a polypeptide, or a molecular complex, or a crystal, as defined above, and a particular compound susceptible to be a ROR-LBD ligand, said process comprising the following steps :

- contacting the said polypeptide, or molecular complex, or crystal, with said particular compound,
- crystallisation of the complex formed between the said polypeptide, or molecular complex, or crystal, and the tested ligand, especially with the vapour diffusion method, and tridimensional analysis of said complex, especially with the molecular replacement method,
- or tridimensional analysis of said complex in soluble state, by using an appropriate method such as NMR.

The present invention provides crystals of an RORβ-LBD bound to a ligand and to a coactivator peptide, i. e. an RORβ-LBD/ligand/peptide complex. The ligand is stearic acid.

The crystal diffracts to 1.9 Å resolution. The crystal of RORβ-LBD preferably has at least 243 amino acid and preferably comprises amino acid sequence 208 to 451 of rat RORβ. The present invention also provides the structure coordinates of the RORβ-LBD/ligand/peptide complex. The complete coordinates are listed in Table A.

The complete coordinates of crystals of an RORβ-LBD bound to a ligand and to a coactivator peptide, i. e. an RORβ-LBD/ligand/peptide complex, wherein the ligand is retinoic acid are listed in Table B.

The present invention also provides a method for determining at least a portion of the three-dimensional structure of molecules or molecular complexes which contain at least some structurally similar features to the RORβ-LBD. It is preferred that these molecules or molecular complexes comprise at least a part of the ligand-binding site defined by structure coordinates of RORβ-LBD amino-acids Q228, Y229, L234, W259, Q261, C262, A263, Q265, I266, H268, A269, L299, V303, L304, R306, M307, R309, A310, V318, L319, F320, E321, M329, F330, L333, L338, I339, A342, F343, V419, C420, H423, and Y446 according to Table A or a mutant or homologue thereof.

The present invention also provides a computer comprising a computer readable form to the coordinates contained in Table A.

The present invention further provides a binding site in RORβ-LBD for an RORβ-LBD agonist or antagonist ligand as well as methods for designing or selecting agonists, antagonist and/or a selective RORβ receptor modulator (SRORM) of ROR using information about the crystal structures disclosed herein.

The present invention also provides a method in order to crystallize orphan receptors, which permits the determination of the ligand-binding pocket, important for the discovery of agonists and antagonists.

Brief description of the Drawing

Figure 1-Stearate

Figure 2- Nucleotide and polypeptide sequences of rat RORβ LBD.

Figure 3- Sequence of the rat RORβ LBD as cloned, with the secondary structural elements boxed (α helices) or drawn with an arrow (β strands). Sequences of human RORβ LBD, mouse RORα LBD, human RORα LBD, mouse RORγ LBD and human RORγ LBD are also given.

For comparison, the aligned sequence of human RARγ LBD, which was used in order to solve the crystallographic structure is given. Residues involved in stearate binding in the case of RORβ or in trans retinoic acid in the case of human RARγ binding are in bold. Residues within a 4 Å cut-off are surrounded by a cercle.

Figure 4- Ribbon style drawing of the RORβ LBD and the co-activator peptide. The ligand stearate is shown as a ball-and-stick figure

Figure 5- Difference (2Fo-Fc) electron density (1σ).

Figure 6: Detail of the hydrogen bond network formed with the ATRA carboxylate group.

Figure 7: Superposition of stearate and ATRA in the RORβ LBD pocket.

Figure 8: binding and transactivation assays for all-trans retinoic acid

Detailed Description of the Invention

The first crystal structure of the RORβ ligand-binding domain (RORβ-LBD) has been determined to 1.9 Å resolution. Crystals of rat RORβ-LBD were grown from crystallizing solutions containing 0.1 M TrisHCl pH= 8.0 and PEG 6000 15%. X-ray diffraction patterns from the crystals have the symmetry and systematic absences of the orthorhombic space group P212121 with unit cell dimensions a= 52.302 Å b= 58.490 Å and c= 106.036 Å and one molecule per asymmetric unit (Mathews Volume = 2,57 $Å^3Da^{-1}$). The structure was determined by the method of molecular replacement using the structure of the retinoic acid (RARγ-LBD) as the search model.

The complex of RORβ-LBD with sterarate and the co-activator peptide shows the mode of binding of the ligand to the orphan receptor in the agonist conformation.

The following abbreviations are used throughout the application:
A=Ala=Alanine
V=Val=Valine
L=Leu=Leucine
I=Ile=Isoleucine
P=Pro=Proline
F=Phe=Phenylalanine
W=Trp=Tryptophane
M=Met=Methionine
G=Gly=Glycine
S=Ser=Serine
T=Thr=Threonine
C=Cys=Cysteine
Y=Tyr=Tyrosine
N=Asn=Asparagine
Q=Gln=Glutamine
D=Asp=Aspartic acid
E=Glu=Glutamic acid
K=Lys=Lysine
R=Arg=Arginine
H=His=Histidine

"Atom type" refers to the element whose coordinates have been determined. Elements are defined by the first letter in the column.

"X, Y, Z" crystallographically define the atomic position determined for each atom.

" B" is a thermal factor that measures movement of the atom around its atomic center.

"Occ" is an occupancy factor that refers to the fraction of the molecules in which each atom occupies the position specified by the coordinates. A value of "1" indicates that each atom has the same conformation, i.e., the same position, in all molecules of the crystal.

Additional definitions are set forth in the specification where necessary.

The RORβ receptor described herein is intended to include any polypeptide which has the activity of the naturally occuring RORβ. The RORβ and RORβ-LBD contemplated herein includes all vertebrate and mammalian forms such as rat, mouse, pig, goat, horse, guinea pig, rabbit, monkey, orangutan and human. Such terms also include polypeptides that differ from naturally occuring forms of RORβ and RORβ-LBD by having amino acid deletions, substitutions, and additions, but which retain the activity of RORβ and RORβ-LBD, respectively. The crystal structure of the invention preferably contains at least 25%, more preferably at least 50%, more preferably at least 75%, more preferably at least 90%, more preferably at least 95%, more preferably at least 99%, and more preferably all of the coordinates listed in Table A. The crystal of the RORβ-LBD/RORβ-LBD-ligand/RORβ-LBD-ligand-peptide of the invention preferably has the following unit cell dimensions in angstroms: a= 52.302 Å b= 58.490 Å and c= 106.036 Å and an orthorhombic space group P212121.

This includes both agonists or activators and antagonist or inhibitors of the RORβ-LBD.

The peptides referred to herein (e.g., RORβ, RORβ-LBD, and the like) may be produced by any well-known method, including synthetic method, such as solid phase, liquid phase and combination solid/liquid phase syntheses; recombinant DNA methods, including cDNA cloning, optionally combined with site directed mutagenesis; and/or purification of the natural products, optionally combined with enzymatic cleavage methods to produce fragments of naturally occuring proteins.

Advantageously, the crystallizable compositions provided by this invention are amenable to x-ray crystallography. Thus, this invention also provides the three-dimensional structure of the RORβ-LBD/RORβ-LBD ligand peptide complex, particularly the complex of rat RORβ-LBD with stearic acid.

The three-dimensional structure of the RORβ-LBD/ligand complex of this invention is defined by a set of structure coordinates as set forth in Table A. The term " structure coordinates" refers to Cartesian coordinates derived from mathematical equations related to the patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centers) of a RORβ/stearate/peptide complex in crystal form. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are then used to establish the positions of the individual atoms of the complex.

Those of skill in the art will understand that a set of structure coordinates for a receptor or receptor/ligand, or receptor/ligand/ peptide complex or a portion thereof, is a relative set of points that define a shape in three dimensions. Thus, it is possible that an entirely different set of coordinates could define a similar or identical shape. Moreover, slight variations in the individual coordinates will have little effect on overall shape.

The variations in coordinates discussed above may be generated because of mathematical manipulations of the structure coordinates. For example, the structure coordinates set forth in Table A could be manipulated by crystallographic permutations of the structure coordinates, fractionalization of the structure coordinates; integer additions or substractions to sets of the structure coordinates, inversion of the structure coordinates or any combination of the above.

Alternatively, modifications in the crystal structure due to mutations, additions, substitutions, and/or deletions of aminoacids, or other changes in any of the components that make up the crystal could also account for variations in structure coordinates. If such variations are within an acceptable standard error as compared to the original coordinates, the resulting three-dimensional shape is considered to be the same.

Various computational analyses are therefore necessary to determine whether a molecule or molecular complex or a portion thereof is sufficiently similar to all or parts of the RORβ receptor/stearate described above as to be considered the same. Such analyses may be carried out in current software applications, such as the Molecular Similarity application of Quanta (Molecular Simulations Inc., San Diego, CA) version 4.1, and as described in the accompanying User's Guide.

The Molecular Similarity application permits comparisons between different structures, different conformations of the same structure, and different parts of the same structure. The procedure used in Molecular Similarity to compare structures is divided into four steps: 1) load the structures to be compared.; 2) define the atom equivalences in these structures; 3) perform a fitting operation; and 4) analyze the results.

Each structure is identified by a name. One structure is identified as the target (i.e., the fixed structure); all remaining structures are working structures (i.e., moving structures). Since atom equivalency within QUANTA is defined by user input, for the purpose of this invention we will define equivalent atoms as protein backbone atoms (N, Cα, C and O) for all conserved residues between the two structures being compared. We will also consider only rigid fitting operations.

When a rigid fitting method is used, the working structure is translated and rotated to obtain an optimum fit with the target structure. The fitting operation uses an algorithm that computes the optimum translation and rotation to be applied to the moving structure, such that the root mean square difference of the fit over the specified pairs of equivalent atom is an absolute minimum. This number, given in angstroms, is reported by QUANTA.

For the purpose of this invention, any molecule or molecular complex that has a root mean square deviation of conserved residue backbone atoms (N, Cα, C, O) of less than 1.5 Å when superimposed on the relevant backbone atoms described by structure coordinates listed in Table A are considered identical. More preferably, the root mean square deviation is less than 1 Å. In a preferred embodiment of the present invention , the molecule or molecular complex comprises at least a portion of the ligand binding site defined by structure coordinates of RORβ-LBD amino acids Q228, Y229, L234, W259, Q261, C262, A263, Q265, I266, H268, A269, L299, V303, L304, R306, M307, R309, A310, V318, L319, F320, E321, M329, F330, L333, L338, I339, A342, F343, V419, C420, H423, and Y446 according to Table A, or a mutant or homologue of said molecule or molecular complex. For purposes of the present invention , by " at least a portion of it" it is meant all or any parts of the ligand-binding site defined by these structure coordinates. More preferred are molecules or molecular complexes comprising all or any parts of the ligand-binding site defined by structure coordinates of RORβ-LBD amino acids Q228, Y229, L234, W259, Q261, C262, A263, Q265, I266, H268, A269, L299, V303, L304, R306, M307, R309, A310, V318, L319, F320, E321, M329, F330, L333, L338, I339, A342, F343, V419, C420, H423, and Y446 according to Table A, or a mutant or homologue of said molecule or molecular complex. By mutant or homologue of the molecule or molecular complex it is meant a molecule or molecular complex having a binding pocket that has a root mean square deviation from the backbone atoms of said RORβ-LBD amino acids of not more than 1.5 Angstroms.

The term "root mean square deviation" means the square root of the arithmetic mean of the squares of deviations from the mean. It is a way to express the deviation or variation from a trend or object. For purposes of this invention, the "root mean square deviation" defines the variation in the backbone of a protein or protein complex from the relevant portion of the backbone of the RORβ portion of the complex as defined by the structure coordinates described herein. Once the structure coordinates of a protein crystal have been determined they are useful in solving the structures of other crystals or in modelling by homology other proteins particularly the two isotypes RORα and γ.

Thus, in accordance with the present invention, the structure coordinates of a RORβ/stearate/peptide complex, and in particular a complex, and portions thereof is stored in a machine-readable storage medium. Such data may be used for a variety of purposes, such as drug discovery and x-ray crystallographic analysis or protein crystal.

Accordingly, in one embodiment of this invention is provided a machine-readable data storage medium comprising a data storage material encoded with the structure coordinates set forth in Table A.

For the first time, the present invention permits the use of structure-based or rational drug design techniques to design, select, and synthesize chemical entities, including

inhibitory and stimulatory compounds that are capable of binding to RORβ-LBD, or any portion thereof.

One particularly useful drug design technique enabled by this invention is iterative drug design. Iterative drug design is a method for optimizing associations between a protein and a compound by determining and evaluating the three-dimensional structures of successive sets of protein/compound complexes.

Those of skill in the art will realize that association of natural ligands or substrates with the binding pockets of their corresponding receptors or enzymes in the basis of many biological mechanisms of action. The term "binding pocket" as used herein, refers to a region of a molecule or molecular complex, that, as a result of its shape, favorably associates with another chemical entity or compound. Similarly, many drugs exert their biological effects through association with the binding pockets of receptors and enzymes. Such associations may occur with all or any parts of the binding pockets. An understanding of such associations will help lead to the design of drugs having more favorable associations with their target receptor, and thus, improved biological effects. Therefore, this information is valuable in designing potential ligands or inhibitors of receptors, such as inhibitors of RORβ.

The term "associating with" refers to a condition of proximity between chemical entities or compounds, or portions thereof. The association may be non-covalent--wherein the juxtaposition is energetically favored by hydrogen bonding or van der Waals or electrostatic interactions -- or it may be covalent.

In iterative drug design, crystals of a series of protein/compound complexes are obtained and then the three-dimensional structures of each complex is solved. Such an approach provides insight into the association between the proteins and compounds of each complex. This is accomplished by selecting compounds with inhibitory activity, obtaining crystals of this new protein/compound complex, solving the three dimensional structure of the complex, and comparing the associations between the new protein/compound complex and previously solved protein/compound complexes. By observing how changes in the compound affected the protein/compound associations, these associations may be optimized.

In some cases, iterative drug design is carried out by forming successive protein-compound complexes and then crystallizing each new complex. Alternatively, a preformed protein crystal is soaked in the presence of an inhibitor, thereby forming a protein/ compound complex and obviating the need to crystallize each individual protein/compound complex.

As used herein, the term "soaked" refers to a process in which the crystal is transferred to a solution containing the compound of interest.

The structure coordinates set forth in Table A can also be used to aid in obtaining structural information about another crystallized molecule or molecular complex. This may be achieved by any of a number of well-known techniques, including molecular replacement.

The structure coordinates set forth in Table A can also be used for determining at least a portion of the three-dimensional structure of molecules or molecular complexes which contain at least some structurally similar features to RORβ. In particular, structural information about another crystallized molecule or molecular complex may be obtained. This may be achieved by any of a number of well-known techniques, including molecular replacement.

Therefore, in another embodiment this invention provides a method of utilizing molecular replacement to obtain structural information about a crystallized molecule or molecular complex whose structure is unknown comprising the steps of:

a) generating an X-ray diffraction pattern from said crystallized molecule or molecular complex,

b) applying at least a portion of the structure coordinates set forth in Table A to the X-ray diffraction pattern to generate a three-dimensional electron density map of the molecule or molecular complex whose structure is unknown; and

c) using all or a portion of the structure coordinates set forth in Table A to generate homology models of RORβ-LBD or any other nuclear orphan or hormone receptor ligand-binding domain.

By using molecular replacement, all or part of the structure coordinates of the RORβ-LBD/RORβ-LBD-ligand/RORβ-LBD-ligand-peptide complex provided by this invention or molecular complex whose structure is unknown more quickly and efficiently than attempting to determine such information ab initio.

Molecular replacement provides an accurate estimation of the phases for an unknown structure. Phases are factors in equations used to solve crystal structures that cannot be determined directly. Obtaining accurate values for the phases, by methods other than molecular replacement, is a time-consuming process that involves iterative cycles of approximations and refinements and greatly hinders the solution of crystal structures. However, when the crystal structure of a protein containing at least a homologous portion has been solved, the phases from the known structure provide a satisfactory estimate of the phases for the unknown structure.

Thus, this method involves generating a preliminary model of a molecule or molecular complex whose structure coordinates are unknown, by orienting and positioning the relevant portion of the RORβ-LBD/RORβ-LBD ligand complex according to Table A within the unit cell of the crystal of the unknown molecule or molecular complex so as best to account for the observed X-ray diffraction pattern of the cristal of the molecule or molecular complex whose structure is unknown. Phases can then be calculated from this model and combined with the observed X-ray diffraction pattern amplitudes to generate an electron density map of the structure whose coordinates are unknown. This, in turn, can be subjected to any well-known model building and structure refinement techniques to provide a final, accurate structure of the unknown crystallized molecule or molecular complex [E. Lattman, "Use of the Rotation and Translation Functions", in Meth. Enzymol., 115, pp55-77 (1985); M. G. Rossmann, ed., "The Molecular Replacement Method", Int. Sci. Rev. Set., No 13, Gordon & Breach, New York (1972)].

The structure of any portion of any crystallized molecule or molecular complex that is sufficiently homologous to any portion of the RORβ-LBD/RORβ-LBD ligand complex can be solved by this method.

The structure coordinates are also particularly useful to solve the structure of crystals of RORβ-LBD/RORβ-LBD ligand or RORβ-LBD ligand peptide co-complexed with a variety of chemical entities. This approach enables the determination of the optimal sites for interaction between chemical entities, including interaction of candidate RORβ inhibitors with the complex. For example, high resolution X-ray diffraction data collected from crystals exposed to different types of solvent allows the determination of where each type of solvent molecule resides. Small molecules that bind tightly to theses sites can then be designed and synthesized and tested for their RORβ inhibition activity.

All of the complexes referred to above may be studied using well-known X-ray difraction techniques and may be refined versus 1.5-3 Å resolution X-ray data to an R-value of about 0.20 or less using computer software, such as X-PLOR [Yale University, 1992, distributed by Molecular Simulations, Inc.; see, e.g., Blundell & Johnson, supra; Meth. Enzymol., vol. 114 & 115, H. W. Wyckoff et al., eds., Academic Press (1985)]. This information may thus be used to optimize known RORβ agonists/antagonists, and more importantly, to design new RORβ agonists/antagonists.

Accordingly, the present invention is also directed to a binding site in RORβ-LBD agonist or antagonist ligand in which a portion of RORβ-LBD ligand is in van der Waals contact or hydrogen bonding contact with at least one of the following residues: Q228, Y229, L234, W259, Q261, C262, A263, Q265, I266, H268, A269, L299, V303, L304, R306, M307, R309, A310, V318, L319, F320, E321, M329, F330, L333, L338, I339, A342, F343, V419, C420, H423, and Y446 of RORβ-LBD. For purposes of this invention, by RORβ-LBD binding site it is also meant to include mutants or homologues thererof. In a preferred embodiment, the mutants or homologues have at least 25% identity, more preferably 50% identity, more preferably 75% identity, and most preferably 95% identity to residues Q228, Y229, L234, W259, Q261, C262, A263, Q265, I266, H268, A269, L299, V303, L304, R306, M307, R309, A310, V318, L319,

F320, E321, M329, F330, L333, L338, I339, A342, F343, V419, C420, H423, and Y446 of RORβ-LBD binding sites.

The present invention is also directed to a machine readable data storage medium, comprising a data storage material encoded with machine readable data, wherein the data is defined by the structure coordinates of an RORβ-LBD/RORβ-LBD ligand according to Table A or a homologue of said complex, wherein said homologue comprises backbone atom that have a root mean square deviation from the backbone atoms of the complex of not more than 3.0 Å. Preferably, the machine readable data storage medium, according to the invention, is wherein said molecule or molecular complex is defined by the set of structure coordinates for RORβ-LBD/RORβ-LBD ligand according to Table A, or a homologue of said molecule or molecular complex, said homologue having a root mean square deviation from the backbone atoms of said aminoacids of not more than 2.0 Å. In a preferred embodiment the machine readable data storage medium comprises a data storage medium comprising a data storage material encoded with a first set of machine readable data comprising a Fourier transform of at least a portion of the structural coordinates for a RORβ-LBD/ RORβ-LBD ligand/ RORβ-LBD ligand peptide according to Table A; which, when combined with a second set of machine readable data comprising an X-ray diffraction pattern of a molecule or molecular complex of unknown structure, using a machine programmed with instructions for using said first set of data and said second set of data, can determine at least a portion of the structure coordinates corresponding to the second set of machine readable data, said first set of data and said second set of data.

The present invention also provides for computational methods using three dimensional models of the RORβ receptor that are based on crystals of RORβ-LBD/RORβ-LBD ligand complex. Generally the computational method of designing an RORβ ligand determines which amino acid or amino acids of the RORβ-LBD interact with a chemical moiety (at least one) of the ligand using a three dimensional model of a crystallized protein comprising the RORβ-LBD with a bound ligand, and selecting a chemical modification (at least one) of the chemical moiety to produce a second chemical moiety with a structure that either decreases or increases an interaction between the interacting amino acid and the second chemical moiety compared to the interaction between the interacting amino acid and the corresponding chemical moiety on the natural hormone.

The computational methods of the present invention are for designing RORβ synthetic ligands using such crystal and three dimensional structural information to generate synthetic ligands that modulate the conformational changes of the RORβ LBD. These computational methods are particularly useful in designing an antagonist or partial agonist to the RORβ, wherein the antagonist or partial agonist has an extended moiety that prevents any one of a number of ligand-induced molecular events that alter the receptor's influence on the regulation of gene expression, such as preventing the normal coordination of the activation domain observed for a naturally occuring ligand or other ligands that mimic the naturally occuring ligand, such as an agonist. As described herein, synthetic ligands of the RORβ receptor will be useful in modulating RORβ activity in a variety of medical conditions.

RORβ is known to comprise various domains as follows:

1) a variable amino-terminal domain;
2) a highly conserved DNA-binding domain (DBD); and
3) a less conserved carboxyl-terminal ligand-binding domain (LBD).

This modularity permits different domains of each protein to separately accomplish different functions, although the domains can influence each other. The separate function of a domain is usually preserved when a particular domain is isolated from the remainder of the protein. Using conventional protein chemistry techniques a modular domain can sometimes be separated from the parent protein. Using conventional molecular biology techniques each domain can usually be separately expressed with its original function intact or chimeraes of two different nuclear receptors can be constructed, wherein the chimerae retain the properties of the individual functional domains of the respective nuclear receptors from which the chimerae were generated.

Amino-Terminal Domain

The amino-terminal domain is the least conserved of the three domains. This domain is involved in transcriptional activation and in some cases its uniqueness may dictate selective receptor-DNA binding and activation of target genes by specific receptors isoforms. This domain can display synergistic and antagonistic interactions with the domains of the LBD. For example, studies with mutated and/or deleted receptors show positive cooperativity of the amino and carboxy terminal domains.

In some cases, deletion of either of these domains will abolish the receptor's transcriptional activation functions.

DNA-Binding Domain

The DBD is the most conserved domain. The DBD contains two perpendicularly oriented α-helices that extend from the base of the first and second zinc fingers. The two zinc fingers function in concert along with non-zinc finger residues to direct nuclear receptors to specific target sites on DNA and to align receptor homodimer to heterodimer interfaces. Various amino acids in DBD influence spacing between two half sites for receptor dimer binding.

Ligand-binding domain

The LBD is the second most highly conserved domain. Whereas integrity of several different LBD sub-domains is important for ligand binding, truncated molecules containing only the LBD retain normal ligand-binding activity. This domain also participates in other functions, including dimerization, nuclear translocation and transcriptional activation. Importantly, this domain binds the ligand and undergoes ligand-induced conformational changes as detailed herein.

As described herein, the LBD of RORβ can be expressed, crystallized, its three dimensional structure determined with a ligand bound (either using crystal data from the same receptor or a different receptor or a combination thereof), and computational methods used to design ligands to its LBD, particularly ligands that contain an extension moiety that coordinates the activation domain of RORβ.

Once a computationaly designed ligand (CDL) is synthesized, it can be tested using assays to establish its activity as an agonist, partial agonist or antagonist, and affinity, as described herein. After such testing, the CDLs can be further refined by generating LBD crystals with a CDL bound to the LBD. The structure of the CDL can then be further refined using the chemical modification methods described herein for three dimensional models to improve the activity or affinity of the CDL and make a second generation CDLs with improved properties, such as that of a super agonist or antagonist.

Typically RORβ-LBD is purified to homogeneity for crystallisation. Purity of RORβ-LBD is measured with SDS-PAGE and mass spectrometry. The purified RORβ for crystallization should be at least 97.5% pure or 97.5% pure, preferably at least 99.0% pure or 99.0% pure, more preferably at least 99.5% pure or 99.5% pure.

Initially purification of the receptor can be obtained by conventional techniques, such as affinity chromatography and gel filtration chromatography.

To achieve higher purification for improved crystals of RORβ, it will be desirable to ligand shift purify the nuclear receptor using a column that separates the receptor according to charge, such as an ion exchange or hydrophobic interaction column, and then bind the eluted receptor with a ligand, especially an agonist. The ligand induces a change in the receptor's surface charge such that when rechromatographed on the same column, the receptor then elutes at the position of the liganded receptor and is removed by the original column run with the unliganded receptor. Usually saturating concentrations of ligand are used in the column and the protein can be preincubated with the ligand prior to passing it over the column.

Some developed methods involve engineering a "tag" such as with histidine placed on the end of the protein, such as on the amino terminus, and then using a cobalt chelation column for purification, Chaga, G., Biotech. Appl. Biochem. 29: 13811-13814 (1991) incorporated by reference.

To determine the three dimensional structure of a RORβ-LBD, it is desirable to co-crystallize the LBD with a corresponding LBD ligand.

Typically purified RORβ-LBD is equilibrated at a saturating concentration of ligand at a temperature that preserves the integrity of the protein. Ligand equilibration can be established between 2 and 37°C, although the receptor tends to be more stable in the 2-20°C range.

However if the ligand is unknown it is possible to co-crystallize the RORβ-LBD with a fortuitous ligand coming from the heterologous expression system i.e. *Escherichia coli* and by adding concomitantly a co-activator peptide.

Preferably crystals are made with the hanging drop methods. Regulated temperature control is desirable to improve crystal stability and quality. Temperatures between 4 and 25°C are generally used and it is often preferable to test crystallization over a range of temperatures. It is preferable to use crystallization temperatures from 18°C to 25°C, more preferably 20 to 23°C, and most preferably 22°C.

Ligands that interact with RORβ can act as agonists, antagonists and partial agonists based on what ligand-induced conformational changes take place.

Agonists induce changes in receptors that place them in an active conformation that allows them to influence transcription, either positively or negatively. There may be several different ligand induced changes in the receptor's conformation.

Antagonists, bind to receptors, but fail to induce conformational changes that leads to the receptor's transcriptionally active form or physiologically relevant conformations. Binding of an antagonist can also block the binding and therefore the actions of an agonist.

Partial agonists bind to receptors and induce only part of the changes in the receptors that are induced by agonists. The differences can be qualitative or quantitative. Thus, a partial agonist may induce some of the conformation changes induced by agonists, but not others, or it may only induce certain changes to a limited extent.

As described herein, the unliganded receptor is in a configuration that is either inactive, has some activity or has repressor activity. Binding of agonist ligands induces conformational changes in the receptor such that the receptor becomes more active, either to stimulate or repress the expression of the genes. The receptors may also have non-genomic actions, some of the known types of changes and/or the sequences of these are listed herein.

Ligand binding by the receptor is a dynamic process, which regulates receptor function by inducing an altered conformation.

The three-dimensional structure of the liganded RORβ receptor will greatly aid in the development of new RORβ synthetic ligands. In addition, RORβ is overall well suited to modern methods including three dimensional structure elucidation and combinatorial chemistry such as those disclosed in EP 335 628, U.S. patent 5, 463,564, which are incorporated herein by reference. Computer programs that use crystallographic data when practising the present invention will enable the rational design of ligand to RORβ.

Programs such as RASMOL can be used with the atomic coordinates from crystals generated by practicing the invention or used to practice the invention by generating three dimensional models and/or determining the structures involved in ligand binding. Computer program such as INSIGHT and GRASP allow further manipulation and the ability to introduce new structures. In addition, high throughput binding and bioactivity assays can be devised using purified recombinant protein and modern reporter gene transcription assays described herein and known in the art in order to refine the activity of a CDL.

Generally, the computational method of designing a RORβ synthetic ligand comprises two steps:

1) determining which amino acid or amino acids of RORβ-LBD interacts with a first chemical moiety (at least one) of the ligand using a three dimensional model of a crystallized protein comprising an RORβ-LBD with a bound ligand; and

2) selecting a chemical modifications (at least one) of the first chemical moiety to produce a second chemical moiety with a structure to either increase or decrease an interaction between the interacting amino acid and the second chemical moiety

compared to the interaction between the interacting amino acid and the first chemical moiety.

Preferably the method is carried out wherein said three dimensional model is generated by comparing isomorphous ligand derivatives to produce improved phasing. Also preferred is wherein said selecting uses said first chemical moiety that interacts with at least one of the interacting amino acids Q228, Y229, L234, W259, Q261, C262, A263, Q265, I266, H268, A269, L299, V303, L304, R306, M307, R309, A310, V318, L319, F320, E321, M329, F330, L333, L338, I339, A342, F343, V419, C420, H423 or Y446.

As shown herein, interacting amino acids form contacts with the ligand and the center of the atoms of the interacting amino acids are usually 2 to 4 angstroms away from the center of the atoms of the ligand. Generally these distances are determined by computer as discussed herein and in Mc Ree 1993, however distances can be determined manually once the three dimensional model is made. See also Renaud et al., Nature 378, 681-689 (1995) for stereochemical figures of three dimensional models.

More commonly, the atoms of the ligand and the atoms of interacting amino acids are 3 to 4 angstroms apart. The invention can be practiced by repeating step 1 and 2 to refine the fit of the ligand to the LBD and to determine a better ligand, such as an agonist. The three dimensional model of RORβ can be represented in two dimensions to determine which amino acids contact the ligand and to select a position on the ligand for chemical modification and changing the interaction with a particular amino acid compared to that before chemical modification. The chemical modification may be made using a computer, manually using a two dimensional representation of the three dimensional model or by chemically synthesizing the ligand. The ligand can also interact with distant amino acids after chemical modification of the ligand to create a new ligand. Distant amino acids are generally not in contact with the ligand before chemical modification. A chemical modification can change the structure of the ligand to make a new ligand that interacts with a distant amino acid usually at least 4.5 angstroms away from the ligand, preferably whereinsaid first chemical moiety is 6 to 12 angstroms away from a distant amino acid. Often distant amino acids will not line the surface of the binding activity for the ligand, they are too far away from the ligand to be part of a pocket or binding cavity. The interaction between a LBD amino acid and an atom of an LBD ligand can be made by any force or attraction described in nature. Usually the interaction between the atom of the amino acid and the ligand will be the result of a hydrogen bonding interaction , charge interaction, hydrophobic interaction, van der Waals interaction or dipole interaction. In the case of the hydrophobic interaction it is recognized that is not a per se interaction between the amino acid and ligand, but rather the usual result, in part, of the repulsion of water or other hydrophilic group from a hydrophobic surface. Reducing or enhancing the interaction of the LBD and a ligand can be measured by calculating or testing binding energies, computationally or using thermodynamic or kinetic methods as known in the art.

Chemical modifications will often enhance or reduce interactions of an atom of a LBD amino acid and an atom of an LBD ligand. Steric hindrance will be a common means of changing the interaction of the LBD cavity with the activation domain.

The present invention also provides methods for identifying compounds that modulates RORβ activity. Various methods or combination thereof can be used to identify these compounds. For example, test compounds can be modeled that fit spatially into the RORβ-LBD as defined by structure coordinates according to Table A, or using a three-dimensional structural model of RORβ-LBD, mutant RORβ-LBD, or RORβ-LBD homolog or portion thereof. Structure coordinates of the ligand binding site, in particular amino acids Q228, Y229, L234, W259, Q261, C262, A263, Q265, I266, H268, A269, L299, V303, L304, R306, M307, R309, A310, V318, L319, F320, E321, M329, F330, L333, L338, I339, A342, F343, V419, C420, H423, or Y446 can also be used to identify structural and chemical features. Identified structural or chemical features can then be employed to design or select compounds as potential RORβ modulators. By structural and chemical features it is meant to include, but is not limited to, van der Waals interactions, hydrogen bonding interactions, charge

interaction, hydrophobic bonding interaction, charge interaction, hydrophobic interaction and dipole interaction. Alternatively, or in conjunction, the three-dimensional structural model or the ligand binding site can be employed to design or select compounds as potential RORβ modulators. Compounds identified as potential RORβ modulators can then be synthesized and screened in an assay characterized by binding of a test compound to the RORβ-LBD. Examples of assays useful in screening of potential ROR modulators include, but are not limited to screening in silico, *in vitro* assays and high throughput assays. Finally, these methods may also involve modifying or replacing one or more amino acids from RORβ-LBD such as Q228, Y229, L234, W259, Q261, C262, A263, Q265, I266, H268, A269, L299, V303, L304, R306, M307, R309, A310, V318, L319, F320, E321, M329, F330, L333, L338, I339, A342, F343, V419, C420, H423, or Y446 of RORβ-LBD according to Table A.

A preferred method of the invention can be described as a computational method of designing an ROR antagonist from an ROR receptor agonist comprising:

1) determining a structure of a molecular recognition domain of said agonist using a three dimensional model of a crystallized protein comprising an RORLBD, and

2) selecting at least one chemical modification of said agonist that provides a ligand structure that extends beyond a binding site for said agonist and in the direction of at least one protein domain important in RORβ biological function.

Another preferred method of the invention can be described as a computational method of designing a selective RORβ receptor modulator such as a ROR receptor super agonist or antagonist comprising:

1) determining at least one interacting amino acid of an RORβ-LBD that interacts with at least one first chemical moiety of said ligand using a three dimensional model of a crystallized protein comprising RORβ-LBD with a bound ligand, and

2) selecting at least one chemical modification of said first chemical moiety to produce a second chemical moiety with a structure to reduce or enhance an interaction between said interacting amino acid and said second chemical moiety compared to said interaction between said interacting amino acid and said first chemical moiety.

However, as will be understood by those of skill in the art upon this disclosure, other structure based design methods can be used. Various computational structure based design methods have been disclosed in the art.

For example, a number computer modeling systems are available in which the sequence of the RORβ-LBD and the RORβ-LBD structure (i.e., atomic coordinates of RORβ-LBD and/or the atomic coordinates of the ligand binding site, the bond and dihedral angles, and distances between atoms in the active site such as provided in Table A) can be input. This computer system then generates the structural details of the site in which a potential RORβ modulator binds so that complementary structural details of the potential modulators can be determined. Design in these modeling systems is generally based upon the compound being capable of physically and structurally associating with RORβ-LBD. In addition, the compound must be able to assume a conformation that allows it to associate with RORβ-LBD. Some modeling systems estimate the potential inhibitory or binding effect of a potential ROR modulator prior to actual synthesis and testing.

Methods for screening chemical entities or fragments for their ability to associate with RORβ-LBD are also well known. Often these methods begin by visual inspection of the active site on the computer screen. Selected fragments or chemical entities are then positioned with the RORβ-LBD. Docking is accomplished using software such as QUANTA and SYBYL, following by energy minimization and molecular dynamics with standard molecular mechanic forcefields such as CHARMM and AMBER. Examples of computer programs which assist in the selection of chemical fragment or chemical entities useful in the present invention include, but are not limited to, GRID (Goodford, P. J.J. Med. Chem. 1985 28: 849-857), AUTODOCK (Goodsell, D.S. and Olsen, A.J. Proteins, Structure, Functions, and Genetics 1990 8: 195-202), and DOCK (Kunts et al. J. Mol. Biol. 1982 161:269-288).

Upon selection of preferred chemical entities or fragments, their relationship to each other and RORβ-LBD can be visualized and then assembled into a single potential

modulator. Programs useful in assembing the individual chemical entities include, but are not limited to CAVEAT (Bartlett et al. Molecular Recognition in Chemical and Biological Problems Special Publication, Royal Chem. Soc. 78, 00. 182-196 (1989) and 3D Database systems (Martin, Y.C. J. Med.Chem. 1992 35:2145-2154).

Alternatively, compounds may be designed de novo using either an empty active site or optionaly including some portion of a known inhibitor. Methods of this type of design include, but are not limited to LUDI (Bohm H-J, J. Comp. Aid. Molec. Design 1992 6:61-78) and LeapFrog (Tripos Associates, St. Louis MO).

The present invention is also directed to a RORβ-LBD selective RORβ modulator (SRORM), in particular an agonist or antagonist, identified by a computational process of the invention.

The present invention is further directed to a method for treating a ROR related disease comprising administering an effective amount of an antagonist identified by a computational process of the invention.

The present invention is also direct to a method for treating a ROR related disease comprising administering an effective amount of an agonist identified by a computational process of the invention.

Compounds identified as agonists, antagonists or SRORMs by the methods disclosed herein which are active when given orally can be formulated as liquids for example syrups, suspensions or emulsions, tablets, capsules and lozenges. A liquid composition will generally consist of a suspension or solution of the compound in a suitable liquid carrier(s), for example ethanol, glycerin, sorbitol, non-aqueous solvent such as polyethlene glycol, oils or water, with a suspending agent, preservative, surfactant, wetting agent, flavoring or coloring agent.

Alternatively, a liquid formulation can be prepared from a reconstitutable powder. For example a powder containing active compound, suspending agent, sucrose and a sweetener can be reconstituted with water to form a suspension; a syrup can be prepared from a powder containing active ingredient, sucrose and a sweetener. A composition in the form of a tablet can be prepared from a powder containing active ingredient, sucrose and a sweetener. A composition in the form of a tablet can be prepared using any suitable pharmaceutical carrier(s) routinely used for preparing solid compositions. Examples of such carriers include magnesium stearate, starch, lactose, sucrose, microcrystalline cellulose, binders, for example polyvinylpyrrolidone. The tablet can also be provided witha color film coating, or colorincluded as part of the carrier(s). In addition, active compound can be formulated in a controlled release dosage form as a tablet comprising a hydrophilic or hydrophobic matrix. A composition in the form of a capsule can be prepared using routine encapsulation procedures, for example by incorporation of active compound and excipients into a hard gelatin capsule. Alternatively, a semi-solid matrix of active compound and high molecular weight polyethylene glycol can be prepared and filled into a hard gelatin capsule; or a solution of active compound in polyethylene glycol or a suspension in edible oil, for example liquid paraffin or fractionated coconut oil can be prepared and filled into a soft gelatin capsule. Compounds identified by the processes described herein which are active when given parenterally can be formulated for intramuscular or intravenous administration. A typical composition for intra-muscular administration will consist of a suspension or solution of active ingredient in an oil, for example arachis oil or sesame oil. A typical composition for intravenous administration will consist of a sterile isotonic aqueous solution containing , for example active ingredient, dextrose, sodium chloride, a co-solvent, for example polyethylene glycol and, optionally, a chelating agent, for example, sodium metabisulphite.

Alternatively, the solution can be freeze dried and then reconstituted with a suitable solvent just prior to administration. Identified compounds which are active on rectal administration can be formulated as suppositories. A typical suppository formulation will generally consist of active ingredient with a binding and/or lubricating agent such as a gelatin or cocoa butter or other low melting vegetable or synthetic wax or fat. Identified compounds which are active on topical administration can be formulated as transdermal compositions. Such compositions include, for example, a backing, active

compound reservoir, a control membrane, liner and contact adhesive. The typical daily dose of a varies according to individual needs, the condition to be treated and with the route of administration. Suitable doses are in the general range of 0.001 to 10mg/kg bodyweight of the recipient per day.

The following examples are to illustrate the invention, but should not be interpreted as a limitation thereon.

Examples

Cloning, Expression and Purification of the RORβ Ligand-Binding Domain

A cDNA for expression of the ligand-binding domain of the rat RORβ-LBD (RORβ-LBD) was constructed using the pet15b vector (Novagen) to include an N-terminal polyhistidine tag and a thrombin cleavage site. *E. coli* BL21 (DE3) cells were grown in LBM at 37 °C to an OD 0.6 and induced with 0.8mM IPTG. The incubation was maintained at 16 °C overnight. Cells were harvested ans stored at -20°C. A total of 6-9 mg of recombinant RORβ-LBD was isolated from a 6 gram cell pellet following sonication and chromatography on a cobalt-chelate resin. Polyhistidine-tagged RORβ-LBD of approximately 90% purity eluted in a gradient of 0 to 1M imidazole. Gel filtration was performed with a Superdex S-200 Hiload 16:60 from Pharmacia. Polyhistidine-tagged rRORβ-LBD of more than 95% purity and homogeneity as checked by SDS-PAGE was concentrated to 5.8 mg/ml in 20mM TrisHCl pH=8.5, 5mMDTT, 2 mM Chaps and 100mM NaCl.

Crystallization

The RORβ-LBD stearate complex was crystallized at 22°C by vapor diffusion in the hanging-drop mode. In the crystallisation trials, the protein was used without further purification and co-crystallized with a 3-molar excess of SRC-1$^{686-700}$(RHKILHRLLQEGSPS) NR-interacting peptide co-activator sequence. Addition of the peptide was crucial to obtain crystals.In the initial trial to obtain crystallization conditions, a sparse matrix crystallization screen was done with a home screen. For each crystallization trial, a 4 µl drop was prepared by mixing 2 µl of purified protein (5.8 mg/ml) with an equal volume of reservoir solution. The reservoir contained 500 µl of the precipitating solution. A crystal measuring 110 x 60 x 30 mm at 22 °C in PEG 6000 15% and 100 mM Tris HCl at pH=8.0 grew within about 2 weeks. This crystal was used in a first data collection run (as described below).

Data Collection and Reduction

The crystals were cryoprotected by equilibration in 15 % PEG 6000 at pH 8.0 containing 15 % glycerol and then flash frozen in liquid ethane at liquid nitrogen temperature. X-ray diffraction data were collected at liquid nitrogen temperature from a single frozen crystal at the ID14-3 beamline at the ESRF Grenoble, France. Crystals diffracted Xrays to a resolution limit of 1.9 Å. All data were integrated and scaled using DENZO and SCALEPACK (Otwinowski and Minor, 1997). The data set between 30 and 3.4 Å shows a completeness of 88.9 % resolution with an Rsym (I) of 2.5. The completeness on high resolution (between 3.4 and 1.9) was 99.8 % with an Rsym (I) of 3.3. The unit cell parameters were a= 52.302 Å b= 58.490 Å and c= 106.036 Å, a=b=c=90°. The crystal was composed by one monomer per asymetric unit, has a solvent content of 52%, and one molecule per asymmetric unit (Mathews Volume = 2.57 $Å^3$ Da^{-1}) The estimated B factor by Wilson plot is 29. Inspection of systematic absences along each axis indicated that the space group was orthorhombic P212121.

Table 1: Data Collection and Processing

Source	Grenoble ID14-3
No of crytals	1
Wavelength	0.93100 Å
Frames	331
$\Delta\Phi$	1°
Crystal to plate distance	260mm
Time/frame	5sec(low res);20sec (high res)
Number of Observations	28846
Data Reduction Program	HKL
Unique reflections	26336
Reflections Used	26331
Resolution	30.0-1.9
Completeness	100
Multiplicity	1
Mosaicity	0.5
^{a}Rsym	3.6 % (15%)
Space group	P212121
a	52.302 Å
b	58.490 Å
c	106.036 Å
Wilson B-value	28.78 Å^2

In the data collection, the last shell values are presented between parentheses.

Structure Determination (Molecular Replacement)

The structure of the complex was solved by molecular replacement using the program AmoRe (Navaza, 1994) and the RARγ holo-LBD (Protein Data Bank accession code, 2lbd) as a search model. The top solution had a correlation coefficient of 27.8 (next highest solution 26.2) and an R factor of 52.7 after AMoRe rigid-body refinement. A solution could also be found with RAR anta as a search model according to the following values: correlation coefficient of 21.4 (next highest solution 19.8) and an R factor of 55.9.

Table 2: Molecular Replacement Statistics

Search Model:	holo-RARγ (PDB file 2LBD)
Program used	AMoRe
Resolution Range	15-3.0 Å
Number of Reflections	4338
Number of Atoms	2011
RF Correlation (first solution)	18.8
TF Correlation (first solution)	24.3
TF R-factor (first solution)	57.0
Rigid Body Correlation	26.0
Rigid Body R-factor	56.7

Structure Refinement

The automated model building Arp/wARP (Perrakis A. et al., 1999) combined with iterative structure refinement was used and permit us to obtain 3 chains constructed which correspond to 243 residues and a connectivity index of 0.98. The calculated electron density maps 3Fo-2Fc delivered Rcryst= 0.2703 and a Rfree = 0.2644.

A partial model of the monomer was build using the graphic program O (Jones et al., 1991) and subjected to alternating rounds of rigid body refinement with X-PLOR (Brünger, 1996) and manual building. The final steps, using cycles of positional

refinement, manual rebuilding, the torsion slow-cool procedure from the program X-PLOR, and individual isotropic B factor refinement delivered Rcryst = 0.2238 and a Rfree =0.2494. The final model refined at 1.9 Å, comprises 244 residues, one ligand, a peptide of 10 amino-acid residues, and 146 water molecules. According to Procheck (Laskowski et al., 1993) 93.2% of all residues in the model are in the most favoured main chain torsion angles Ramachandran regions, 5.9% in addtional allowed regions, 0.4% in generously allowed regions and 0.4% are in disallowed regions. These last percentages corresponds to two residues (D403 and E404) situated in the loop 9-10, which did not present a well defined density.

Table 3: Final Refinement Parameters

Resolution Range	30.0-1.9
Reflections	26331
R-factor	22.4%
R-free	24.9%
# residues	201-452 (207)
# atoms	1977
RMS deviations	
bond lengths	0.008
bond angles	1.282
Average B-factors	
Protein	29.5 $Å^2$
Stearate	47.9 $Å^2$
Water	39.8 $Å^2$

Description of the Molecule

The structure of RORβ-LBD is complete from residues 208 through 451.

Analysis of the structure with program Procheck showed only minor exeptions to the allowed geometry. In the structure, the first seven residues of the chain (201-207) are not seen in the electron density map and are probably disordered. This leaves only one residue before the initial residue of the first α-helix (H1) in the wild-type structure. On the C-terminal end, only the last residue (452) is not seen in the electron density map. The loop between helices H9 and H10 (residues N399 and E405) is not well defined.

Folding and packing

As expected, the RORβ-LBD has the same overall three-dimensional structure as those of the other nuclear hormone receptor LBDs. The molecule is folded into a "helical sandwich" consisting of 10 α-helices. There are two small pieces of beta strand, forming a short beta sheet located in the core of the molecule between helices 5 and 6 near the ligand binding site. Helix 12 is folded toward the ligand binding domain core. Its last turn comes in close contact to H4, H11 and the co-activator peptide. An interaction surface comprising residues from the H3-H4 region and H12 allows the co-activator peptide to bind.

The following sequence of the peptide is seen in the crystal structure: HKILHRLLQE. The LXXLL motif also called the NR-box is included in an amphipathic α-helix interacting with a hydrophobic cleft on the LBD surface. In particularly, the side-chains of Leu 693 and Leu 694 are part of an hydrophobic cluster composed also by Val 274 (H3), Ile 292 (H4), and Leu 295 (H4).

The γ carboxylate of E448 (H12) forms hydrogen bonds with the backbone amides of Leu 697 and Leu 698, residues of N-terminal turn of the peptide helix. This N-capping interaction was already described (Nolte & al., 1998, Shiau et al., 1998). This highly conserved glutamate residue is known to be important for transactivation. Another hydrogen bond requires Gln 288 (H4) OE2 with NE2 of His 695. The side chain of Glu 700 forms a water-mediated hydrogen bond to the carbonyl of residue Arg 696.

Binding of stearate

The volume of the ligand binding pocket is 758 $Å^3$, which is close to that of VDR (660 $Å^3$) (Rochel et al. , 2000). A fortuitous ligand, stearic acid, was found in the ligand binding pocket, which was previously characterized by mass spectrometry. Thus, it appears that *E. coli*-endogeneous stearic acid was co-purified and co-crystallised with the heterologously expressed RORβ LBD. The fatty acid (FA) is buried in a predominantly hydrophobic pocket formed by residues located in H3 (Gln 265, Ile 266, Ala269), H5 (Leu 300, Val303, Leu97), loop H5-H6 (Phe 113), H6 (Phe 320), and H7 (Leu131, Val338). Most of these residues make van der Waals contact with the aliphatic chain of the FA (Figure 3a). The cavity contains also 11 ordered water molecules. One oxygen atom of the carboxylate group forms hydrogen bond with NE2 of Gln265. This residue varies among RORα and β. The other oxygen atom of the carboxylate group forms hydrogen bond with two ordered water molecules. These two molecules are part of a hydrogen bond network, which connects the carboxylate to other conserved residues among RORα and β of the LBP namely Gln228 and Arg306. Stearate adopts a U-shaped conformation upon binding.

Table 4: Stearate contacts (3.5 Å)

Hydrogen bonds					
O2	Gln 265 Nε2	2.79Å			
O1	Wat 944		2.54Å O	Val 303	3.11Å
Possible Close Contacts					
O1	Ala 269 Cβ		3.31Å		
O2	Gln 265 Cγ		3.33Å		
O2	Gln 265 Cδ		3.41Å		
O2	Wat 946		3.06 Å		
C3	Wat 944		3.43 Å		
C3	Wat 946		3.21 Å		
C4	Wat 946		3.30 Å		
C10	Phe 123 CE1	3.43 Å			
C11	Leu 131 CD2	3.45 Å			

crystallization and structure determination of the RORβ LBD/ATRA (all-*trans* retinoic acid) complex

As mentioned above, the RORβ LBD construct where the two C-terminal solvent-exposed cysteines have been removed by truncation of a 7-residue C-terminal segment has proved a valuable tool to get other crystal structures of the RORβ LBD in complex with other ligands. This is illustrated below with the description of the crystallization and the structure determination of the RORβ LBD/ATRA (all-*trans* retinoic acid) complex. This new structure reveals another mode of binding for the ligand and suggests that natural and synthetic retinoids are candidate ligands for RORβ. This family of compounds may thus be tested for binding to the RORβ LBD, for instance by mass spectrometry, and the crystallization may be tried in the positive cases. From the obtained structures, high-affinity ligands can be designed, synthetized, and tested *in vivo*, *in vitro*, as well as for crystallization. Even without the crystal structure of other complexes, filtering for ligand screening and/or design of better ligands can be achieved through docking studies *in computo*.

Crystallization of the RORβ LBD/ATRA complex

The RORβ LBD/ATRA complex was crystallized by vapor diffusion in the hanging-drop mode. The protein (the RORβ LBD containing stearic acid, purified as previously) was co-crystallised with an excess ATRA and an excess SRC-1 (residues 686-700) under similar conditions as for the RORβ LBD/STE (stearic acid) complex. A 4 µl drop

was prepared by mixing 2 µl of purified protein (5.8 mg/ml) with an equal volume of reservoir solution. The reservoir (500 µl) contained 18% PEG 6000 and 100 mM Tris HCl pH=8.0. A crystal measuring 300x 160 x 100 µm grew within 2 weeks at 22°C.

Data Collection

The crystals were cryoprotected with a film of viscous paraffin oil and then flash frozen in liquid ethane at liquid nitrogen temperature. X-ray diffraction data were collected at liquid nitrogen temperature from a single frozen crystal at the BM14-CRG beamline at the ESRF Grenoble, France. Crystals diffracted X-rays to a resolution limit of 2.1 Å. All data were integrated and scaled using DENZO and SCALEPACK (Table 5). The data set between 20.0 and 2.1 Å shows a completeness of 100 % with an Rsym (I) of 4.5%. The completeness in the highest resolution shell (2.17-2.10 Å) was 100 % with an Rsym (I) of 17.5%. The unit cell parameters were a=52.199Å, b=58.125Å, and c=106.039Å, a=b=c=90°. The crystal contains one monomer per asymetric unit and a solvent content of 52%. The estimated B factor by Wilson plot is 32. Inspection of systematic absences along each axis indicated that the space group was P212121.

Structure Determination and Refinement

The structure of the complex was solved by molecular replacement using the RORβ LBD/STE complex as a starting model. The all-*trans* retinoic acid was built using Quanta (MSI). The final model (Rcryst = 0.2180 and Rfree =0.2549), refined at 2.1 Å (Table 5), comprises 244 residues from the RORβ LBD, 10 residues from the peptide, one ligand, and 139 water molecules. According to Procheck, 91.2% of all residues in the model are in the most favoured main chain torsion angles Ramachandran regions, 5.9% in additional allowed regions, 2.1% in generously allowed regions and 0.0% in disallowed regions.

Binding of ATRA (all-*trans* retinoic acid)

The protein-ligand contacts within 3.5 Å are listed in Table 6. The present structure reveals the binding site for the carboxylate group of ATRA, which is hydrogen-bonded to Arg 306 and Arg 309 through a water molecule in each case (Figure 6). The binding mode is different from that of stearate (Figure 7), which is hydrogen-bonded to Gln 265 directly and to Gln 228 through a water molecule. On the other hand, stearate makes more Van der Waals contacts with pocket residues thanks to its flexible chain which assumes a U shape probably in order to maximize the number of such contacts. ATRA is more rigid, allowing less Van der Waals contacts. Thus, there seems to be a delicate balance between Van der Waals contacts and hydrogen bonds ligand binding to the RORβ LBD.

Table 5: Data collection and refinement statistics.

Source	ESRF BM14
Wavelength	0.976205 Å
Unique reflections	19431
Resolution range	20.0- 2.1
[a]Completeness	100 % (100 %)
Multiplicity	6.6
Mosaicity	0.75°
[a]Rsym	4.5 % (17.5%)
Space group	P212121
a	52.199 Å
b	58.125 Å
c	106.039 Å

[a]The last shell values are presented between parentheses.

Resolution Range	20.0-2.1
Reflections	17679
R-factor	21.8%
R-free	25.5%
# visible residues	244 (residues 208-451)
# atoms	2219
RMS deviations	
bond lengths	0.007
bond angles	1.129
Average B-factors	
Protein and peptide	33.6 Å^2
All-trans retinoic acid	40.3 Å^2
Water	43.2 Å^2
Wilson B-factor	31.9 Å^2

Table 6: RORβ LBD / ATRA (all-*trans* retinoic acid) contacts within 3.5 Å

Hydrogen bonds		
O1	N Gln 228	2.97 Å
O1	Wat 802	2.72 Å
O2	Wat 825	2.59 Å
NH1	Arg 306	2.92 Å
NH1	Arg 309	2.84 Å
Van der Waals contacts		
O1	Arg 306 Cδ	3.50 Å
O2	Tyr 229 N	3.42 Å
O2	Gln 228 N	3.42 Å
C15	Gln 228 N	3.48 Å
C15	Wat 825	3.39 Å
C18	Cys 262 Cβ	3.42 Å
C18	Cys 262 Sγ	3.44 Å
C19	Leu 319 O	3.34 Å
C20	Wat 825	3.22 Å

Cell Culture and Transient Transfection Experiments.
HT22 were cultured in in Dulbecco's modified Eagle's medium (DMEM). The Medium was supplemented with 5% delipidated fetal calf serum, penicillin, streptomycin and glutamine. Transient transfection assays were carried out in 24-well plates (0.5 10^5 cells per well) *N*-[1-(2,3-dioleoyloxy)propyl]-*N,N,N*-trimethylammoniummethylsulfate (DOTAP) lipofection (Roche Molecular Biochemicals) according to the manufacturer's protocol. Luciferase activity was assayed as recommended by the manufacturer (Promega) in a Microplate Luminometer (EG & G Berthold). Relative light units were

normalized according to (Muller et al., 2002) and protein concentration was determined using the Bradford dye assay (Bio-Rad). All experiments were repeated at least five times.

Ligands. Purchased ligands include the following: *all-trans*-[20-methyl-3H]-retinoic acid (65 Ci/mmol) (NEN); *all-trans*-retinoic acid (Sigma)
Recombinant plasmids. *Reporter plasmids.* G5E1BTataLuc
Expression vectors. CMX-Gal, CMX-Gal-RORß201-459, pGEX-RORß201-459 described in (Greiner et al., 1996)

Ligand binding assays. Scintillation proximity assay were performed with purified bacterial expressed RORß-LBD (stehlin et al 2001) (250 ng per well) and *all-trans*-[20-methyl-3H]-retinoic acid (60 Ci/mMol, NEN) in 96-well NiNTA-flash-plates (NEN) in a total volume of 100 µl. Binding buffer: 40 mM HEPES pH 7.6, 40 mM KCl, 0.2 % CHAPS, 0.1 mg/ml BSA. Binding was carried out for 1 hour at 4°C in 100 µl binding buffer. Radioligand was diluted in binding buffer to a final concentration of 5 nM. Unlabelled competing ligands were serially diluted in binding buffer and added at final concentrations ranging from 1 nM to 10 µM. Plates were shaken at 25°C for 2 hours. Then the radioactivity was measured with a Packard Topcount at 2 min per well. All concentrations were assayed in triplicate and the results were averaged. Values from wells void of competitor represented 100% binding. Saturation-binding experiments used the ligand concentrations indicated in the figure. Nonspecific binding was determined by including unlablled retinoic acid at 10^{-4} M and subtracted from total binding. Nonlinear regression analysis for the competition curves, saturation binding and Scratchard analysis to determine the Kd were performed using GRAPHPAD PRISM.

Greiner, E. F., Kirfel, J., Greschik, H., Dorflinger, U., Becker, P., Mercep, A., and Schule, R. (1996). Functional analysis of retinoid Z receptor beta, a brain-specific nuclear orphan receptor. Proc Natl Acad Sci U S A *93*, 10105-10110.
Muller, J. M., Metzger, E., Greschik, H., Bosserhoff, A. K., Mercep, L., Buettner, R., and Schule, R. (2002). The transcriptional coactivator FHL2 transmits Rho signals from the cell membrane into the nucleus. Embo J *21*, 736-748.

TABLE A: Crystallographic Coordinates of RORbeta LBD/stearic acid/SRC1 peptide complex

ATOM	1	CB	THR	208	14.051	-0.802	26.838	1.00	36.55
ATOM	2	OG1	THR	208	15.478	-0.898	26.824	1.00	35.48
ATOM	3	CG2	THR	208	13.533	-0.599	25.404	1.00	36.95
ATOM	4	C	THR	208	14.780	1.393	27.790	1.00	35.14
ATOM	5	O	THR	208	15.234	1.884	26.757	1.00	33.86
ATOM	6	N	THR	208	12.302	0.901	27.332	1.00	33.90
ATOM	7	CA	THR	208	13.631	0.366	27.747	1.00	34.84
ATOM	8	N	MET	209	15.261	1.697	28.997	1.00	35.20
ATOM	9	CA	MET	209	16.358	2.647	29.169	1.00	34.91
ATOM	10	CB	MET	209	16.717	2.770	30.658	1.00	34.61
ATOM	11	CG	MET	209	17.482	4.050	31.032	1.00	35.43
ATOM	12	SD	MET	209	16.609	5.601	30.589	1.00	35.84
ATOM	13	CE	MET	209	15.558	5.830	32.022	1.00	33.07
ATOM	14	C	MET	209	17.598	2.235	28.346	1.00	34.50
ATOM	15	O	MET	209	18.313	3.100	27.813	1.00	34.32
ATOM	16	N	SER	210	17.846	0.930	28.225	1.00	32.92
ATOM	17	CA	SER	210	18.999	0.456	27.461	1.00	33.75
ATOM	18	CB	SER	210	19.181	-1.064	27.604	1.00	34.40
ATOM	19	OG	SER	210	18.057	-1.784	27.107	1.00	37.86
ATOM	20	C	SER	210	18.886	0.821	25.983	1.00	32.54
ATOM	21	O	SER	210	19.888	1.145	25.345	1.00	32.59
ATOM	22	N	GLU	211	17.684	0.746	25.422	1.00	31.57
ATOM	23	CA	GLU	211	17.525	1.121	24.020	1.00	30.40
ATOM	24	CB	GLU	211	16.125	0.782	23.484	1.00	30.37
ATOM	25	CG	GLU	211	15.813	1.507	22.160	1.00	32.71
ATOM	26	CD	GLU	211	14.495	1.097	21.511	1.00	34.29
ATOM	27	OE1	GLU	211	13.563	0.690	22.233	1.00	34.92
ATOM	28	OE2	GLU	211	14.384	1.205	20.267	1.00	34.73

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ATOM     29  C   GLU   211      17.752   2.625  23.883  1.00 28.59
ATOM     30  O   GLU   211      18.351   3.080  22.913  1.00 27.98
ATOM     31  N   ILE   212      17.264   3.396  24.848  1.00 27.40
ATOM     32  CA  ILE   212      17.424   4.845  24.781  1.00 27.79
ATOM     33  CB  ILE   212      16.764   5.571  25.978  1.00 26.35
ATOM     34  CG2 ILE   212      17.010   7.069  25.860  1.00 27.12
ATOM     35  CG1 ILE   212      15.257   5.276  26.029  1.00 26.58
ATOM     36  CD1 ILE   212      14.503   5.643  24.770  1.00 24.95
ATOM     37  C   ILE   212      18.895   5.226  24.757  1.00 27.70
ATOM     38  O   ILE   212      19.302   6.124  24.021  1.00 26.95
ATOM     39  N   ASP   213      19.691   4.530  25.563  1.00 29.11
ATOM     40  CA  ASP   213      21.122   4.800  25.653  1.00 29.22
ATOM     41  CB  ASP   213      21.699   4.045  26.853  1.00 32.21
ATOM     42  CG  ASP   213      23.083   4.517  27.233  1.00 34.57
ATOM     43  OD1 ASP   213      23.255   5.721  27.529  1.00 36.05
ATOM     44  OD2 ASP   213      24.004   3.674  27.248  1.00 37.52
ATOM     45  C   ASP   213      21.873   4.430  24.365  1.00 28.75
ATOM     46  O   ASP   213      22.804   5.137  23.954  1.00 27.10
ATOM     47  N   ARG   214      21.475   3.329  23.732  1.00 28.19
ATOM     48  CA  ARG   214      22.108   2.908  22.480  1.00 29.03
ATOM     49  CB  ARG   214      21.597   1.535  22.047  1.00 32.44
ATOM     50  CG  ARG   214      21.849   0.417  23.050  1.00 38.05
ATOM     51  CD  ARG   214      21.039  -0.810  22.667  1.00 41.57
ATOM     52  NE  ARG   214      20.958  -1.777  23.759  1.00 46.23
ATOM     53  CZ  ARG   214      20.771  -3.082  23.582  1.00 49.23
ATOM     54  NH1 ARG   214      20.644  -3.577  22.346  1.00 50.85
ATOM     55  NH2 ARG   214      20.720  -3.894  24.632  1.00 50.33
ATOM     56  C   ARG   214      21.785   3.928  21.383  1.00 27.33
ATOM     57  O   ARG   214      22.624   4.236  20.543  1.00 26.60
ATOM     58  N   ILE   215      20.559   4.446  21.391  1.00 26.45
ATOM     59  CA  ILE   215      20.150   5.432  20.395  1.00 24.84
ATOM     60  CB  ILE   215      18.629   5.699  20.472  1.00 26.20
ATOM     61  CG2 ILE   215      18.280   7.043  19.821  1.00 25.14
ATOM     62  CG1 ILE   215      17.881   4.554  19.781  1.00 25.45
ATOM     63  CD1 ILE   215      16.422   4.458  20.176  1.00 25.36
ATOM     64  C   ILE   215      20.929   6.723  20.629  1.00 24.62
ATOM     65  O   ILE   215      21.426   7.338  19.686  1.00 23.32
ATOM     66  N   ALA   216      21.050   7.116  21.893  1.00 24.39
ATOM     67  CA  ALA   216      21.782   8.323  22.242  1.00 25.02
ATOM     68  CB  ALA   216      21.677   8.589  23.740  1.00 24.99
ATOM     69  C   ALA   216      23.249   8.232  21.829  1.00 25.36
ATOM     70  O   ALA   216      23.778   9.151  21.193  1.00 25.93
ATOM     71  N   GLN   217      23.922   7.137  22.177  1.00 25.23
ATOM     72  CA  GLN   217      25.332   6.999  21.819  1.00 26.24
ATOM     73  CB  GLN   217      25.917   5.705  22.397  1.00 29.19
ATOM     74  CG  GLN   217      26.090   5.734  23.917  1.00 35.04
ATOM     75  CD  GLN   217      27.010   4.630  24.420  1.00 38.21
ATOM     76  OE1 GLN   217      26.714   3.443  24.278  1.00 40.35
ATOM     77  NE2 GLN   217      28.140   5.022  25.006  1.00 41.77
ATOM     78  C   GLN   217      25.556   7.041  20.305  1.00 25.19
ATOM     79  O   GLN   217      26.518   7.651  19.823  1.00 24.32
ATOM     80  N   ASN   218      24.659   6.392  19.568  1.00 23.86
ATOM     81  CA  ASN   218      24.725   6.341  18.113  1.00 23.77
ATOM     82  CB  ASN   218      23.580   5.472  17.591  1.00 23.58
ATOM     83  CG  ASN   218      23.554   5.381  16.084  1.00 24.49
ATOM     84  OD1 ASN   218      22.492   5.461  15.480  1.00 24.92
ATOM     85  ND2 ASN   218      24.723   5.194  15.466  1.00 26.45
ATOM     86  C   ASN   218      24.632   7.746  17.508  1.00 23.84
ATOM     87  O   ASN   218      25.430   8.122  16.642  1.00 23.34
ATOM     88  N   ILE   219      23.654   8.518  17.967  1.00 23.13
ATOM     89  CA  ILE   219      23.464   9.872  17.462  1.00 22.12
ATOM     90  CB  ILE   219      22.116  10.448  17.948  1.00 20.95
ATOM     91  CG2 ILE   219      22.033  11.927  17.630  1.00 18.97
ATOM     92  CG1 ILE   219      20.975   9.653  17.300  1.00 20.42
ATOM     93  CD1 ILE   219      19.602   9.904  17.878  1.00 21.20
ATOM     94  C   ILE   219      24.615  10.784  17.874  1.00 22.86
ATOM     95  O   ILE   219      25.132  11.552  17.063  1.00 21.51
ATOM     96  N   ILE   220      25.020  10.693  19.132  1.00 22.66
ATOM     97  CA  ILE   220      26.128  11.503  19.616  1.00 24.02
ATOM     98  CB  ILE   220      26.418  11.199  21.098  1.00 23.77
ATOM     99  CG2 ILE   220      27.801  11.712  21.479  1.00 25.51
ATOM    100  CG1 ILE   220      25.323  11.824  21.970  1.00 24.25
ATOM    101  CD1 ILE   220      25.371  11.402  23.442  1.00 25.63
ATOM    102  C   ILE   220      27.379  11.217  18.783  1.00 24.51
ATOM    103  O   ILE   220      28.070  12.133  18.338  1.00 24.01
ATOM    104  N   LYS   221      27.655   9.937  18.563  1.00 25.74
ATOM    105  CA  LYS   221      28.826   9.538  17.796  1.00 26.09
ATOM    106  CB  LYS   221      28.987   8.017  17.845  1.00 27.05
ATOM    107  CG  LYS   221      30.069   7.447  16.940  1.00 30.22
ATOM    108  CD  LYS   221      30.218   5.948  17.211  1.00 33.17
ATOM    109  CE  LYS   221      30.998   5.233  16.112  1.00 35.08
ATOM    110  NZ  LYS   221      32.350   5.814  15.948  1.00 37.04
ATOM    111  C   LYS   221      28.724  10.027  16.352  1.00 26.19
ATOM    112  O   LYS   221      29.710  10.504  15.783  1.00 26.37
ATOM    113  N   SER   222      27.538   9.932  15.765  1.00 24.31
ATOM    114  CA  SER   222      27.365  10.388  14.389  1.00 24.58
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ATOM	115	CB	SER	222	25.947	10.105	13.894	1.00	25.00
ATOM	116	OG	SER	222	25.818	10.539	12.544	1.00	27.88
ATOM	117	C	SER	222	27.654	11.882	14.278	1.00	23.15
ATOM	118	O	SER	222	28.312	12.332	13.340	1.00	20.13
ATOM	119	N	HIS	223	27.160	12.640	15.254	1.00	22.79
ATOM	120	CA	HIS	223	27.369	14.081	15.292	1.00	23.51
ATOM	121	CB	HIS	223	26.694	14.672	16.530	1.00	22.71
ATOM	122	CG	HIS	223	27.071	16.095	16.803	1.00	22.35
ATOM	123	CD2	HIS	223	27.948	16.627	17.686	1.00	23.97
ATOM	124	ND1	HIS	223	26.531	17.158	16.114	1.00	23.67
ATOM	125	CE1	HIS	223	27.055	18.284	16.561	1.00	22.61
ATOM	126	NE2	HIS	223	27.918	17.990	17.516	1.00	24.30
ATOM	127	C	HIS	223	28.860	14.408	15.334	1.00	24.83
ATOM	128	O	HIS	223	29.348	15.233	14.570	1.00	23.29
ATOM	129	N	LEU	224	29.581	13.758	16.239	1.00	26.00
ATOM	130	CA	LEU	224	31.005	14.012	16.378	1.00	27.42
ATOM	131	CB	LEU	224	31.564	13.241	17.579	1.00	28.17
ATOM	132	CG	LEU	224	31.065	13.762	18.936	1.00	29.44
ATOM	133	CD1	LEU	224	31.630	12.901	20.062	1.00	30.81
ATOM	134	CD2	LEU	224	31.482	15.226	19.118	1.00	31.36
ATOM	135	C	LEU	224	31.791	13.686	15.116	1.00	27.94
ATOM	136	O	LEU	224	32.777	14.358	14.823	1.00	28.46
ATOM	137	N	GLU	225	31.352	12.676	14.366	1.00	26.53
ATOM	138	CA	GLU	225	32.042	12.289	13.138	1.00	28.08
ATOM	139	CB	GLU	225	31.897	10.785	12.867	1.00	29.02
ATOM	140	CG	GLU	225	31.994	9.881	14.083	1.00	32.55
ATOM	141	CD	GLU	225	31.914	8.410	13.714	1.00	34.16
ATOM	142	OE1	GLU	225	31.093	8.046	12.822	1.00	35.71
ATOM	143	OE2	GLU	225	32.666	7.615	14.322	1.00	33.88
ATOM	144	C	GLU	225	31.540	13.028	11.897	1.00	26.89
ATOM	145	O	GLU	225	32.105	12.862	10.820	1.00	27.36
ATOM	146	N	THR	226	30.499	13.845	12.032	1.00	26.42
ATOM	147	CA	THR	226	29.959	14.540	10.860	1.00	25.86
ATOM	148	CB	THR	226	28.574	13.972	10.486	1.00	24.69
ATOM	149	OG1	THR	226	27.670	14.165	11.579	1.00	21.37
ATOM	150	CG2	THR	226	28.684	12.478	10.162	1.00	25.22
ATOM	151	C	THR	226	29.850	16.067	10.890	1.00	26.84
ATOM	152	O	THR	226	29.016	16.645	10.196	1.00	25.61
ATOM	153	N	CYS	227	30.670	16.719	11.698	1.00	27.47
ATOM	154	CA	CYS	227	30.677	18.177	11.733	1.00	29.95
ATOM	155	CB	CYS	227	30.725	18.694	13.160	1.00	30.26
ATOM	156	SG	CYS	227	29.129	18.666	13.964	1.00	31.37
ATOM	157	C	CYS	227	31.927	18.614	10.993	1.00	31.15
ATOM	158	O	CYS	227	32.949	17.926	11.044	1.00	32.10
ATOM	159	N	GLN	228	31.856	19.737	10.291	1.00	32.99
ATOM	160	CA	GLN	228	33.028	20.217	9.559	1.00	34.05
ATOM	161	CB	GLN	228	32.700	21.472	8.746	1.00	34.74
ATOM	162	CG	GLN	228	33.975	22.087	8.166	1.00	36.23
ATOM	163	CD	GLN	228	33.732	23.051	7.040	1.00	36.08
ATOM	164	OE1	GLN	228	34.591	23.216	6.172	1.00	37.80
ATOM	165	NE2	GLN	228	32.579	23.710	7.049	1.00	35.92
ATOM	166	C	GLN	228	34.163	20.543	10.527	1.00	34.44
ATOM	167	O	GLN	228	35.345	20.276	10.254	1.00	35.97
ATOM	168	N	TYR	229	33.794	21.134	11.656	1.00	33.42
ATOM	169	CA	TYR	229	34.762	21.508	12.664	1.00	34.12
ATOM	170	CB	TYR	229	34.804	23.025	12.814	1.00	34.64
ATOM	171	CG	TYR	229	35.252	23.753	11.578	1.00	35.84
ATOM	172	CD1	TYR	229	36.530	23.558	11.052	1.00	37.22
ATOM	173	CE1	TYR	229	36.960	24.278	9.925	1.00	37.82
ATOM	174	CD2	TYR	229	34.412	24.667	10.953	1.00	36.84
ATOM	175	CE2	TYR	229	34.823	25.380	9.841	1.00	37.23
ATOM	176	CZ	TYR	229	36.093	25.191	9.333	1.00	38.42
ATOM	177	OH	TYR	229	36.496	25.957	8.260	1.00	40.27
ATOM	178	C	TYR	229	34.420	20.895	14.004	1.00	34.39
ATOM	179	O	TYR	229	33.292	21.045	14.489	1.00	33.47
ATOM	180	N	THR	230	35.385	20.202	14.601	1.00	35.45
ATOM	181	CA	THR	230	35.151	19.622	15.913	1.00	37.95
ATOM	182	CB	THR	230	36.301	18.697	16.373	1.00	38.23
ATOM	183	OG1	THR	230	37.502	19.463	16.518	1.00	40.39
ATOM	184	CG2	THR	230	36.522	17.593	15.370	1.00	39.49
ATOM	185	C	THR	230	35.074	20.807	16.851	1.00	38.40
ATOM	186	O	THR	230	35.466	21.927	16.488	1.00	37.62
ATOM	187	N	MET	231	34.555	20.567	18.049	1.00	40.09
ATOM	188	CA	MET	231	34.421	21.614	19.055	1.00	42.13
ATOM	189	CB	MET	231	33.812	21.031	20.319	1.00	42.86
ATOM	190	CG	MET	231	32.379	21.368	20.493	1.00	44.14
ATOM	191	SD	MET	231	32.214	22.979	21.200	1.00	48.47
ATOM	192	CE	MET	231	31.477	23.899	19.813	1.00	44.81
ATOM	193	C	MET	231	35.761	22.239	19.392	1.00	42.66
ATOM	194	O	MET	231	35.833	23.413	19.754	1.00	42.23
ATOM	195	N	GLU	232	36.817	21.435	19.287	1.00	44.27
ATOM	196	CA	GLU	232	38.176	21.900	19.564	1.00	46.03
ATOM	197	CB	GLU	232	39.159	20.718	19.589	1.00	48.16
ATOM	198	CG	GLU	232	39.075	19.847	20.834	1.00	52.20
ATOM	199	CD	GLU	232	39.978	18.626	20.745	1.00	54.53
ATOM	200	OE1	GLU	232	41.211	18.807	20.581	1.00	55.69

ATOM	201	OE2	GLU	232	39.452	17.483	20.831	1.00	55.83
ATOM	202	C	GLU	232	38.629	22.893	18.484	1.00	45.35
ATOM	203	O	GLU	232	39.137	23.971	18.785	1.00	45.45
ATOM	204	N	GLU	233	38.449	22.506	17.227	1.00	44.58
ATOM	205	CA	GLU	233	38.837	23.341	16.099	1.00	43.02
ATOM	206	CB	GLU	233	38.530	22.625	14.780	1.00	43.47
ATOM	207	CG	GLU	233	39.477	21.486	14.414	1.00	43.69
ATOM	208	CD	GLU	233	39.053	20.792	13.134	1.00	44.50
ATOM	209	OE1	GLU	233	37.937	20.228	13.113	1.00	42.94
ATOM	210	OE2	GLU	233	39.826	20.819	12.144	1.00	45.82
ATOM	211	C	GLU	233	38.130	24.693	16.128	1.00	42.63
ATOM	212	O	GLU	233	38.664	25.689	15.629	1.00	41.56
ATOM	213	N	LEU	234	36.927	24.716	16.702	1.00	41.55
ATOM	214	CA	LEU	234	36.130	25.929	16.800	1.00	41.68
ATOM	215	CB	LEU	234	34.662	25.569	17.081	1.00	38.99
ATOM	216	CG	LEU	234	33.595	25.745	15.984	1.00	37.42
ATOM	217	CD1	LEU	234	34.202	25.811	14.598	1.00	36.02
ATOM	218	CD2	LEU	234	32.598	24.602	16.068	1.00	35.04
ATOM	219	C	LEU	234	36.659	26.884	17.874	1.00	43.02
ATOM	220	O	LEU	234	36.689	28.097	17.665	1.00	42.82
ATOM	221	N	HIS	235	37.063	26.347	19.024	1.00	44.76
ATOM	222	CA	HIS	235	37.609	27.183	20.100	1.00	46.16
ATOM	223	CB	HIS	235	37.997	26.304	21.303	1.00	47.16
ATOM	224	CG	HIS	235	36.823	25.826	22.102	1.00	47.88
ATOM	225	CD2	HIS	235	35.624	26.405	22.363	1.00	48.26
ATOM	226	ND1	HIS	235	36.816	24.615	22.765	1.00	48.61
ATOM	227	CE1	HIS	235	35.664	24.465	23.398	1.00	48.18
ATOM	228	NE2	HIS	235	34.922	25.536	23.169	1.00	48.08
ATOM	229	C	HIS	235	38.833	27.943	19.580	1.00	46.16
ATOM	230	O	HIS	235	39.093	29.086	19.972	1.00	46.99
ATOM	231	N	GLN	236	39.570	27.304	18.676	1.00	46.28
ATOM	232	CA	GLN	236	40.763	27.888	18.078	1.00	46.35
ATOM	233	CB	GLN	236	41.709	26.769	17.647	1.00	48.10
ATOM	234	CG	GLN	236	42.314	26.013	18.819	1.00	50.88
ATOM	235	CD	GLN	236	43.066	24.776	18.378	1.00	53.03
ATOM	236	OE1	GLN	236	42.483	23.846	17.799	1.00	54.30
ATOM	237	NE2	GLN	236	44.368	24.750	18.651	1.00	53.30
ATOM	238	C	GLN	236	40.469	28.804	16.882	1.00	45.38
ATOM	239	O	GLN	236	41.358	29.510	16.401	1.00	45.98
ATOM	240	N	LEU	237	39.231	28.793	16.396	1.00	43.26
ATOM	241	CA	LEU	237	38.864	29.650	15.276	1.00	41.13
ATOM	242	CB	LEU	237	38.032	28.877	14.249	1.00	40.63
ATOM	243	CG	LEU	237	38.733	27.918	13.291	1.00	40.27
ATOM	244	CD1	LEU	237	37.700	27.272	12.379	1.00	39.92
ATOM	245	CD2	LEU	237	39.777	28.674	12.485	1.00	40.45
ATOM	246	C	LEU	237	38.081	30.878	15.727	1.00	39.51
ATOM	247	O	LEU	237	38.086	31.903	15.047	1.00	38.80
ATOM	248	N	ALA	238	37.427	30.778	16.880	1.00	39.51
ATOM	249	CA	ALA	238	36.618	31.871	17.406	1.00	38.91
ATOM	250	CB	ALA	238	35.908	31.423	18.694	1.00	39.73
ATOM	251	C	ALA	238	37.408	33.152	17.656	1.00	38.89
ATOM	252	O	ALA	238	36.832	34.239	17.716	1.00	38.65
ATOM	253	N	TRP	239	38.725	33.041	17.794	1.00	39.18
ATOM	254	CA	TRP	239	39.524	34.239	18.022	1.00	39.10
ATOM	255	CB	TRP	239	40.771	33.912	18.844	1.00	39.97
ATOM	256	CG	TRP	239	40.439	33.575	20.265	1.00	41.05
ATOM	257	CD2	TRP	239	40.329	34.502	21.357	1.00	41.89
ATOM	258	CE2	TRP	239	39.925	33.764	22.496	1.00	42.28
ATOM	259	CE3	TRP	239	40.527	35.889	21.481	1.00	42.04
ATOM	260	CD1	TRP	239	40.111	32.345	20.768	1.00	41.20
ATOM	261	NE1	TRP	239	39.800	32.451	22.113	1.00	41.62
ATOM	262	CZ2	TRP	239	39.718	34.369	23.749	1.00	42.42
ATOM	263	CZ3	TRP	239	40.318	36.495	22.734	1.00	41.71
ATOM	264	CH2	TRP	239	39.917	35.732	23.846	1.00	41.59
ATOM	265	C	TRP	239	39.904	34.917	16.715	1.00	38.66
ATOM	266	O	TRP	239	40.315	36.081	16.708	1.00	39.17
ATOM	267	N	GLN	240	39.750	34.191	15.613	1.00	37.88
ATOM	268	CA	GLN	240	40.052	34.715	14.281	1.00	38.38
ATOM	269	CB	GLN	240	40.402	33.569	13.325	1.00	39.13
ATOM	270	CG	GLN	240	41.815	33.009	13.448	1.00	43.03
ATOM	271	CD	GLN	240	42.865	33.999	12.962	1.00	45.47
ATOM	272	OE1	GLN	240	42.697	34.640	11.913	1.00	46.02
ATOM	273	NE2	GLN	240	43.962	34.121	13.712	1.00	45.97
ATOM	274	C	GLN	240	38.841	35.473	13.726	1.00	38.04
ATOM	275	O	GLN	240	37.750	34.900	13.590	1.00	36.35
ATOM	276	N	THR	241	39.029	36.752	13.406	1.00	37.28
ATOM	277	CA	THR	241	37.938	37.554	12.865	1.00	37.13
ATOM	278	CB	THR	241	37.417	38.596	13.901	1.00	38.89
ATOM	279	OG1	THR	241	38.436	39.565	14.186	1.00	40.81
ATOM	280	CG2	THR	241	37.028	37.907	15.208	1.00	39.48
ATOM	281	C	THR	241	38.347	38.279	11.580	1.00	36.22
ATOM	282	O	THR	241	39.485	38.758	11.451	1.00	36.33
ATOM	283	N	HIS	242	37.430	38.324	10.613	1.00	34.05
ATOM	284	CA	HIS	242	37.695	39.012	9.354	1.00	31.44
ATOM	285	CB	HIS	242	36.472	38.974	8.436	1.00	29.25
ATOM	286	CG	HIS	242	36.149	37.615	7.904	1.00	27.92

ATOM	287	CD2	HIS	242	36.715	36.887	6.915	1.00	26.55
ATOM	288	ND1	HIS	242	35.115	36.853	8.393	1.00	27.30
ATOM	289	CE1	HIS	242	35.055	35.715	7.727	1.00	26.17
ATOM	290	NE2	HIS	242	36.020	35.710	6.826	1.00	27.22
ATOM	291	C	HIS	242	38.020	40.465	9.668	1.00	30.68
ATOM	292	O	HIS	242	37.358	41.096	10.490	1.00	30.78
ATOM	293	N	THR	243	39.038	40.991	9.004	1.00	31.03
ATOM	294	CA	THR	243	39.460	42.372	9.199	1.00	30.79
ATOM	295	CB	THR	243	40.822	42.612	8.543	1.00	30.73
ATOM	296	OG1	THR	243	40.717	42.383	7.126	1.00	31.15
ATOM	297	CG2	THR	243	41.864	41.669	9.140	1.00	29.69
ATOM	298	C	THR	243	38.470	43.363	8.595	1.00	31.03
ATOM	299	O	THR	243	37.534	42.970	7.901	1.00	29.40
ATOM	300	N	TYR	244	38.684	44.648	8.868	1.00	31.19
ATOM	301	CA	TYR	244	37.834	45.702	8.324	1.00	31.95
ATOM	302	CB	TYR	244	38.297	47.095	8.802	1.00	33.18
ATOM	303	CG	TYR	244	37.829	47.457	10.204	1.00	33.91
ATOM	304	CD1	TYR	244	38.719	47.484	11.289	1.00	35.00
ATOM	305	CE1	TYR	244	38.268	47.784	12.599	1.00	35.72
ATOM	306	CD2	TYR	244	36.486	47.736	10.450	1.00	35.64
ATOM	307	CE2	TYR	244	36.025	48.032	11.740	1.00	35.81
ATOM	308	CZ	TYR	244	36.915	48.054	12.809	1.00	36.54
ATOM	309	OH	TYR	244	36.440	48.350	14.072	1.00	36.95
ATOM	310	C	TYR	244	37.894	45.641	6.805	1.00	31.62
ATOM	311	O	TYR	244	36.879	45.842	6.123	1.00	31.91
ATOM	312	N	GLU	245	39.085	45.363	6.280	1.00	30.27
ATOM	313	CA	GLU	245	39.281	45.271	4.841	1.00	30.86
ATOM	314	CB	GLU	245	40.764	45.070	4.502	1.00	32.11
ATOM	315	CG	GLU	245	41.664	46.274	4.773	1.00	34.84
ATOM	316	CD	GLU	245	41.999	46.477	6.248	1.00	36.73
ATOM	317	OE1	GLU	245	42.570	47.548	6.573	1.00	37.44
ATOM	318	OE2	GLU	245	41.710	45.578	7.080	1.00	36.51
ATOM	319	C	GLU	245	38.476	44.105	4.283	1.00	29.31
ATOM	320	O	GLU	245	37.722	44.262	3.325	1.00	28.06
ATOM	321	N	GLU	246	38.632	42.939	4.904	1.00	28.59
ATOM	322	CA	GLU	246	37.921	41.740	4.458	1.00	28.73
ATOM	323	CB	GLU	246	38.360	40.539	5.298	1.00	28.89
ATOM	324	CG	GLU	246	39.841	40.230	5.106	1.00	33.43
ATOM	325	CD	GLU	246	40.377	39.192	6.065	1.00	34.90
ATOM	326	OE1	GLU	246	40.008	39.213	7.259	1.00	36.44
ATOM	327	OE2	GLU	246	41.196	38.363	5.625	1.00	37.65
ATOM	328	C	GLU	246	36.407	41.941	4.515	1.00	26.90
ATOM	329	O	GLU	246	35.690	41.539	3.604	1.00	26.66
ATOM	330	N	ILE	247	35.921	42.580	5.575	1.00	27.96
ATOM	331	CA	ILE	247	34.488	42.838	5.702	1.00	26.28
ATOM	332	CB	ILE	247	34.155	43.539	7.048	1.00	26.69
ATOM	333	CG2	ILE	247	32.729	44.062	7.031	1.00	25.56
ATOM	334	CG1	ILE	247	34.360	42.570	8.222	1.00	25.48
ATOM	335	CD1	ILE	247	33.500	41.318	8.148	1.00	26.47
ATOM	336	C	ILE	247	34.043	43.741	4.546	1.00	27.42
ATOM	337	O	ILE	247	32.977	43.544	3.954	1.00	25.31
ATOM	338	N	LYS	248	34.876	44.723	4.214	1.00	27.71
ATOM	339	CA	LYS	248	34.538	45.638	3.135	1.00	28.31
ATOM	340	CB	LYS	248	35.547	46.786	3.059	1.00	31.00
ATOM	341	CG	LYS	248	34.912	48.072	2.556	1.00	36.20
ATOM	342	CD	LYS	248	34.261	48.862	3.708	1.00	37.72
ATOM	343	CE	LYS	248	33.507	47.965	4.691	1.00	39.77
ATOM	344	NZ	LYS	248	32.922	48.683	5.861	1.00	40.50
ATOM	345	C	LYS	248	34.482	44.914	1.802	1.00	27.15
ATOM	346	O	LYS	248	33.618	45.191	0.972	1.00	25.35
ATOM	347	N	ALA	249	35.404	43.976	1.612	1.00	27.48
ATOM	348	CA	ALA	249	35.462	43.197	0.380	1.00	27.44
ATOM	349	CB	ALA	249	36.639	42.235	0.423	1.00	28.05
ATOM	350	C	ALA	249	34.151	42.427	0.213	1.00	27.33
ATOM	351	O	ALA	249	33.576	42.386	-0.882	1.00	26.70
ATOM	352	N	TYR	250	33.681	41.820	1.303	1.00	26.77
ATOM	353	CA	TYR	250	32.428	41.072	1.272	1.00	26.29
ATOM	354	CB	TYR	250	32.131	40.421	2.628	1.00	26.30
ATOM	355	CG	TYR	250	32.869	39.129	2.881	1.00	26.73
ATOM	356	CD1	TYR	250	32.749	38.051	2.008	1.00	26.93
ATOM	357	CE1	TYR	250	33.416	36.854	2.252	1.00	27.90
ATOM	358	CD2	TYR	250	33.674	38.981	4.007	1.00	27.33
ATOM	359	CE2	TYR	250	34.342	37.788	4.262	1.00	27.78
ATOM	360	CZ	TYR	250	34.210	36.731	3.385	1.00	27.25
ATOM	361	OH	TYR	250	34.878	35.556	3.650	1.00	28.52
ATOM	362	C	TYR	250	31.276	41.997	0.932	1.00	25.31
ATOM	363	O	TYR	250	30.352	41.612	0.230	1.00	24.79
ATOM	364	N	GLN	251	31.324	43.213	1.456	1.00	26.05
ATOM	365	CA	GLN	251	30.261	44.169	1.198	1.00	27.36
ATOM	366	CB	GLN	251	30.311	45.309	2.208	1.00	28.26
ATOM	367	CG	GLN	251	30.146	44.860	3.644	1.00	29.79
ATOM	368	CD	GLN	251	30.114	46.024	4.597	1.00	32.00
ATOM	369	OE1	GLN	251	30.908	46.963	4.465	1.00	33.43
ATOM	370	NE2	GLN	251	29.208	45.972	5.577	1.00	30.11
ATOM	371	C	GLN	251	30.333	44.739	-0.207	1.00	28.15
ATOM	372	O	GLN	251	29.348	45.278	-0.714	1.00	28.35

ATOM	373	N	SER	252	31.498	44.629	-0.835	1.00	28.46
ATOM	374	CA	SER	252	31.670	45.138	-2.195	1.00	29.58
ATOM	375	CB	SER	252	33.115	45.586	-2.408	1.00	29.66
ATOM	376	OG	SER	252	33.399	46.707	-1.587	1.00	33.07
ATOM	377	C	SER	252	31.287	44.087	-3.225	1.00	30.02
ATOM	378	O	SER	252	31.319	44.333	-4.432	1.00	30.26
ATOM	379	N	LYS	253	30.917	42.908	-2.742	1.00	29.52
ATOM	380	CA	LYS	253	30.512	41.827	-3.630	1.00	30.07
ATOM	381	CB	LYS	253	30.421	40.509	-2.854	1.00	30.99
ATOM	382	CG	LYS	253	31.759	39.923	-2.457	1.00	33.63
ATOM	383	CD	LYS	253	32.609	39.683	-3.697	1.00	35.38
ATOM	384	CE	LYS	253	33.918	38.993	-3.352	1.00	38.01
ATOM	385	NZ	LYS	253	33.690	37.648	-2.761	1.00	36.66
ATOM	386	C	LYS	253	29.156	42.120	-4.250	1.00	29.23
ATOM	387	O	LYS	253	28.333	42.815	-3.663	1.00	29.23
ATOM	388	N	SER	254	28.922	41.596	-5.446	1.00	29.17
ATOM	389	CA	SER	254	27.631	41.786	-6.080	1.00	29.19
ATOM	390	CB	SER	254	27.667	41.371	-7.545	1.00	29.22
ATOM	391	OG	SER	254	27.816	39.968	-7.640	1.00	25.88
ATOM	392	C	SER	254	26.710	40.830	-5.341	1.00	29.60
ATOM	393	O	SER	254	27.171	39.862	-4.739	1.00	29.62
ATOM	394	N	ARG	255	25.416	41.097	-5.404	1.00	28.75
ATOM	395	CA	ARG	255	24.430	40.257	-4.749	1.00	29.78
ATOM	396	CB	ARG	255	23.034	40.853	-4.969	1.00	31.17
ATOM	397	CG	ARG	255	21.941	40.222	-4.139	1.00	34.14
ATOM	398	CD	ARG	255	20.773	41.191	-3.965	1.00	37.49
ATOM	399	NE	ARG	255	19.500	40.485	-3.868	1.00	40.31
ATOM	400	CZ	ARG	255	19.100	39.578	-4.755	1.00	41.60
ATOM	401	NH1	ARG	255	19.890	39.287	-5.782	1.00	44.13
ATOM	402	NH2	ARG	255	17.924	38.971	-4.631	1.00	39.96
ATOM	403	C	ARG	255	24.508	38.809	-5.255	1.00	27.97
ATOM	404	O	ARG	255	24.376	37.867	-4.473	1.00	27.13
ATOM	405	N	GLU	256	24.748	38.628	-6.549	1.00	27.81
ATOM	406	CA	GLU	256	24.854	37.284	-7.115	1.00	28.27
ATOM	407	CB	GLU	256	24.876	37.331	-8.647	1.00	29.71
ATOM	408	CG	GLU	256	24.028	38.425	-9.243	1.00	34.67
ATOM	409	CD	GLU	256	24.701	39.784	-9.149	1.00	34.34
ATOM	410	OE1	GLU	256	25.746	39.971	-9.808	1.00	37.48
ATOM	411	OE2	GLU	256	24.193	40.652	-8.417	1.00	34.93
ATOM	412	C	GLU	256	26.121	36.577	-6.639	1.00	27.13
ATOM	413	O	GLU	256	26.106	35.379	-6.379	1.00	26.34
ATOM	414	N	ALA	257	27.221	37.322	-6.543	1.00	26.59
ATOM	415	CA	ALA	257	28.497	36.747	-6.108	1.00	24.46
ATOM	416	CB	ALA	257	29.593	37.789	-6.190	1.00	23.06
ATOM	417	C	ALA	257	28.406	36.210	-4.685	1.00	23.27
ATOM	418	O	ALA	257	28.828	35.084	-4.413	1.00	22.83
ATOM	419	N	LEU	258	27.855	37.015	-3.780	1.00	22.28
ATOM	420	CA	LEU	258	27.743	36.602	-2.386	1.00	22.36
ATOM	421	CB	LEU	258	27.382	37.788	-1.480	1.00	21.42
ATOM	422	CG	LEU	258	27.623	37.516	0.012	1.00	21.16
ATOM	423	CD1	LEU	258	29.104	37.335	0.264	1.00	22.80
ATOM	424	CD2	LEU	258	27.098	38.656	0.857	1.00	22.10
ATOM	425	C	LEU	258	26.712	35.487	-2.253	1.00	22.29
ATOM	426	O	LEU	258	26.921	34.537	-1.498	1.00	21.82
ATOM	427	N	TRP	259	25.608	35.580	-2.990	1.00	21.90
ATOM	428	CA	TRP	259	24.617	34.514	-2.921	1.00	23.48
ATOM	429	CB	TRP	259	23.405	34.801	-3.823	1.00	24.84
ATOM	430	CG	TRP	259	22.260	35.370	-3.052	1.00	28.57
ATOM	431	CD2	TRP	259	21.325	34.637	-2.259	1.00	30.31
ATOM	432	CE2	TRP	259	20.509	35.580	-1.594	1.00	31.88
ATOM	433	CE3	TRP	259	21.101	33.269	-2.039	1.00	31.88
ATOM	434	CD1	TRP	259	21.974	36.692	-2.853	1.00	29.73
ATOM	435	NE1	TRP	259	20.926	36.826	-1.977	1.00	31.45
ATOM	436	CZ2	TRP	259	19.484	35.202	-0.721	1.00	33.37
ATOM	437	CZ3	TRP	259	20.084	32.893	-1.171	1.00	32.58
ATOM	438	CH2	TRP	259	19.288	33.858	-0.520	1.00	33.41
ATOM	439	C	TRP	259	25.279	33.203	-3.328	1.00	23.16
ATOM	440	O	TRP	259	25.066	32.176	-2.695	1.00	23.39
ATOM	441	N	GLN	260	26.094	33.238	-4.378	1.00	24.68
ATOM	442	CA	GLN	260	26.793	32.037	-4.824	1.00	24.94
ATOM	443	CB	GLN	260	27.666	32.352	-6.046	1.00	28.06
ATOM	444	CG	GLN	260	28.451	31.142	-6.568	1.00	34.11
ATOM	445	CD	GLN	260	29.968	31.291	-6.467	1.00	38.33
ATOM	446	OE1	GLN	260	30.524	31.565	-5.390	1.00	39.00
ATOM	447	NE2	GLN	260	30.650	31.084	-7.594	1.00	40.25
ATOM	448	C	GLN	260	27.671	31.473	-3.695	1.00	24.10
ATOM	449	O	GLN	260	27.671	30.269	-3.435	1.00	23.36
ATOM	450	N	GLN	261	28.429	32.342	-3.037	1.00	22.77
ATOM	451	CA	GLN	261	29.302	31.926	-1.940	1.00	23.59
ATOM	452	CB	GLN	261	30.089	33.124	-1.395	1.00	25.53
ATOM	453	CG	GLN	261	31.165	33.672	-2.321	1.00	31.43
ATOM	454	CD	GLN	261	31.847	34.924	-1.754	1.00	35.45
ATOM	455	OE1	GLN	261	31.616	36.053	-2.226	1.00	38.71
ATOM	456	NE2	GLN	261	32.678	34.732	-0.733	1.00	33.46
ATOM	457	C	GLN	261	28.508	31.295	-0.796	1.00	22.79
ATOM	458	O	GLN	261	28.893	30.254	-0.255	1.00	21.63

ATOM	459	N	CYS	262	27.404	31.940	-0.425	1.00	21.36
ATOM	460	CA	CYS	262	26.558	31.437	0.651	1.00	21.18
ATOM	461	CB	CYS	262	25.483	32.453	1.003	1.00	20.56
ATOM	462	SG	CYS	262	26.149	33.886	1.830	1.00	23.42
ATOM	463	C	CYS	262	25.907	30.110	0.287	1.00	20.19
ATOM	464	O	CYS	262	25.800	29.216	1.128	1.00	20.82
ATOM	465	N	ALA	263	25.475	29.977	-0.962	1.00	19.51
ATOM	466	CA	ALA	263	24.855	28.731	-1.391	1.00	20.19
ATOM	467	CB	ALA	263	24.323	28.875	-2.790	1.00	19.19
ATOM	468	C	ALA	263	25.871	27.582	-1.319	1.00	20.32
ATOM	469	O	ALA	263	25.530	26.455	-0.946	1.00	20.47
ATOM	470	N	ILE	264	27.120	27.869	-1.666	1.00	19.64
ATOM	471	CA	ILE	264	28.163	26.844	-1.613	1.00	20.56
ATOM	472	CB	ILE	264	29.479	27.352	-2.233	1.00	21.64
ATOM	473	CG2	ILE	264	30.599	26.336	-2.003	1.00	24.40
ATOM	474	CG1	ILE	264	29.276	27.584	-3.733	1.00	22.79
ATOM	475	CD1	ILE	264	30.506	28.182	-4.453	1.00	23.68
ATOM	476	C	ILE	264	28.411	26.426	-0.169	1.00	19.92
ATOM	477	O	ILE	264	28.490	25.235	0.142	1.00	20.57
ATOM	478	N	GLN	265	28.518	27.408	0.720	1.00	20.33
ATOM	479	CA	GLN	265	28.749	27.108	2.122	1.00	20.30
ATOM	480	CB	GLN	265	28.961	28.392	2.919	1.00	22.53
ATOM	481	CG	GLN	265	29.345	28.128	4.349	1.00	27.06
ATOM	482	CD	GLN	265	30.391	27.024	4.480	1.00	30.59
ATOM	483	OE1	GLN	265	31.470	27.086	3.866	1.00	31.46
ATOM	484	NE2	GLN	265	30.075	26.003	5.286	1.00	31.02
ATOM	485	C	GLN	265	27.584	26.313	2.722	1.00	19.48
ATOM	486	O	GLN	265	27.800	25.335	3.435	1.00	18.61
ATOM	487	N	ILE	266	26.357	26.734	2.427	1.00	18.19
ATOM	488	CA	ILE	266	25.167	26.049	2.933	1.00	19.33
ATOM	489	CB	ILE	266	23.877	26.775	2.494	1.00	19.84
ATOM	490	CG2	ILE	266	22.652	25.925	2.813	1.00	17.56
ATOM	491	CG1	ILE	266	23.797	28.134	3.179	1.00	20.35
ATOM	492	CD1	ILE	266	22.643	28.987	2.693	1.00	21.92
ATOM	493	C	ILE	266	25.137	24.619	2.406	1.00	19.49
ATOM	494	O	ILE	266	24.860	23.681	3.151	1.00	19.71
ATOM	495	N	THR	267	25.427	24.452	1.120	1.00	19.07
ATOM	496	CA	THR	267	25.426	23.117	0.529	1.00	20.39
ATOM	497	CB	THR	267	25.732	23.173	-0.973	1.00	19.62
ATOM	498	OG1	THR	267	24.727	23.949	-1.624	1.00	18.77
ATOM	499	CG2	THR	267	25.747	21.767	-1.577	1.00	19.77
ATOM	500	C	THR	267	26.476	22.239	1.204	1.00	19.70
ATOM	501	O	THR	267	26.240	21.063	1.484	1.00	19.00
ATOM	502	N	HIS	268	27.642	22.823	1.449	1.00	18.99
ATOM	503	CA	HIS	268	28.734	22.113	2.098	1.00	19.17
ATOM	504	CB	HIS	268	29.926	23.063	2.248	1.00	20.12
ATOM	505	CG	HIS	268	31.167	22.409	2.764	1.00	22.30
ATOM	506	CD2	HIS	268	32.052	22.803	3.707	1.00	24.34
ATOM	507	ND1	HIS	268	31.634	21.207	2.279	1.00	24.49
ATOM	508	CE1	HIS	268	32.752	20.887	2.903	1.00	23.24
ATOM	509	NE2	HIS	268	33.029	21.838	3.775	1.00	23.14
ATOM	510	C	HIS	268	28.237	21.616	3.462	1.00	19.37
ATOM	511	O	HIS	268	28.415	20.449	3.811	1.00	19.15
ATOM	512	N	ALA	269	27.587	22.501	4.215	1.00	17.47
ATOM	513	CA	ALA	269	27.050	22.139	5.525	1.00	18.95
ATOM	514	CB	ALA	269	26.522	23.380	6.237	1.00	18.60
ATOM	515	C	ALA	269	25.938	21.090	5.406	1.00	18.49
ATOM	516	O	ALA	269	25.838	20.181	6.229	1.00	19.32
ATOM	517	N	ILE	270	25.104	21.221	4.377	1.00	17.85
ATOM	518	CA	ILE	270	24.017	20.277	4.165	1.00	17.94
ATOM	519	CB	ILE	270	23.113	20.735	2.999	1.00	17.72
ATOM	520	CG2	ILE	270	22.238	19.569	2.502	1.00	15.68
ATOM	521	CG1	ILE	270	22.256	21.914	3.476	1.00	17.69
ATOM	522	CD1	ILE	270	21.442	22.593	2.381	1.00	19.17
ATOM	523	C	ILE	270	24.571	18.883	3.889	1.00	19.48
ATOM	524	O	ILE	270	24.049	17.881	4.377	1.00	17.18
ATOM	525	N	GLN	271	25.644	18.815	3.114	1.00	19.72
ATOM	526	CA	GLN	271	26.229	17.519	2.826	1.00	20.49
ATOM	527	CB	GLN	271	27.376	17.687	1.827	1.00	21.65
ATOM	528	CG	GLN	271	26.832	18.047	0.439	1.00	22.49
ATOM	529	CD	GLN	271	27.895	18.166	-0.646	1.00	23.92
ATOM	530	OE1	GLN	271	27.588	18.037	-1.831	1.00	26.25
ATOM	531	NE2	GLN	271	29.129	18.429	-0.252	1.00	23.47
ATOM	532	C	GLN	271	26.663	16.804	4.118	1.00	20.60
ATOM	533	O	GLN	271	26.516	15.586	4.236	1.00	20.59
ATOM	534	N	TYR	272	27.159	17.552	5.098	1.00	20.89
ATOM	535	CA	TYR	272	27.547	16.940	6.368	1.00	21.15
ATOM	536	CB	TYR	272	28.329	17.933	7.231	1.00	23.11
ATOM	537	CG	TYR	272	29.801	18.001	6.871	1.00	26.45
ATOM	538	CD1	TYR	272	30.637	16.898	7.065	1.00	29.06
ATOM	539	CE1	TYR	272	31.989	16.937	6.702	1.00	31.21
ATOM	540	CD2	TYR	272	30.351	19.153	6.306	1.00	28.01
ATOM	541	CE2	TYR	272	31.705	19.203	5.938	1.00	30.00
ATOM	542	CZ	TYR	272	32.513	18.091	6.140	1.00	31.38
ATOM	543	OH	TYR	272	33.846	18.137	5.786	1.00	34.21
ATOM	544	C	TYR	272	26.312	16.426	7.120	1.00	21.57

ATOM	545	O	TYR	272	26.378	15.401	7.810	1.00	20.19
ATOM	546	N	VAL	273	25.185	17.122	6.973	1.00	18.53
ATOM	547	CA	VAL	273	23.950	16.687	7.623	1.00	18.96
ATOM	548	CB	VAL	273	22.832	17.740	7.496	1.00	18.38
ATOM	549	CG1	VAL	273	21.529	17.186	8.052	1.00	15.65
ATOM	550	CG2	VAL	273	23.229	19.004	8.247	1.00	17.10
ATOM	551	C	VAL	273	23.474	15.365	7.007	1.00	19.57
ATOM	552	O	VAL	273	22.881	14.526	7.687	1.00	20.30
ATOM	553	N	VAL	274	23.731	15.181	5.718	1.00	19.26
ATOM	554	CA	VAL	274	23.352	13.934	5.065	1.00	21.47
ATOM	555	CB	VAL	274	23.595	13.997	3.538	1.00	19.96
ATOM	556	CG1	VAL	274	23.323	12.640	2.914	1.00	22.18
ATOM	557	CG2	VAL	274	22.678	15.052	2.905	1.00	20.72
ATOM	558	C	VAL	274	24.191	12.808	5.685	1.00	21.11
ATOM	559	O	VAL	274	23.668	11.746	6.021	1.00	22.06
ATOM	560	N	GLU	275	25.487	13.062	5.854	1.00	22.26
ATOM	561	CA	GLU	275	26.401	12.088	6.446	1.00	23.73
ATOM	562	CB	GLU	275	27.836	12.632	6.449	1.00	26.76
ATOM	563	CG	GLU	275	28.448	12.827	5.058	1.00	30.97
ATOM	564	CD	GLU	275	29.000	11.534	4.446	1.00	34.75
ATOM	565	OE1	GLU	275	28.264	10.512	4.404	1.00	34.78
ATOM	566	OE2	GLU	275	30.180	11.553	3.995	1.00	37.39
ATOM	567	C	GLU	275	25.954	11.803	7.875	1.00	22.91
ATOM	568	O	GLU	275	26.046	10.674	8.354	1.00	21.80
ATOM	569	N	PHE	276	25.468	12.842	8.547	1.00	21.94
ATOM	570	CA	PHE	276	24.978	12.725	9.915	1.00	21.89
ATOM	571	CB	PHE	276	24.512	14.101	10.412	1.00	20.02
ATOM	572	CG	PHE	276	23.891	14.091	11.790	1.00	20.99
ATOM	573	CD1	PHE	276	24.507	13.431	12.850	1.00	20.12
ATOM	574	CD2	PHE	276	22.722	14.817	12.040	1.00	20.12
ATOM	575	CE1	PHE	276	23.975	13.502	14.144	1.00	21.36
ATOM	576	CE2	PHE	276	22.182	14.895	13.325	1.00	20.21
ATOM	577	CZ	PHE	276	22.808	14.239	14.381	1.00	19.91
ATOM	578	C	PHE	276	23.809	11.741	9.935	1.00	21.78
ATOM	579	O	PHE	276	23.815	10.771	10.688	1.00	22.96
ATOM	580	N	ALA	277	22.813	11.997	9.091	1.00	21.26
ATOM	581	CA	ALA	277	21.626	11.148	9.012	1.00	21.02
ATOM	582	CB	ALA	277	20.650	11.705	7.979	1.00	19.08
ATOM	583	C	ALA	277	21.968	9.700	8.671	1.00	21.78
ATOM	584	O	ALA	277	21.450	8.774	9.294	1.00	22.63
ATOM	585	N	LYS	278	22.836	9.511	7.683	1.00	23.13
ATOM	586	CA	LYS	278	23.240	8.173	7.256	1.00	25.28
ATOM	587	CB	LYS	278	24.209	8.275	6.078	1.00	24.01
ATOM	588	CG	LYS	278	23.561	8.837	4.803	1.00	26.41
ATOM	589	CD	LYS	278	24.575	8.997	3.689	1.00	24.85
ATOM	590	CE	LYS	278	25.265	7.676	3.395	1.00	25.80
ATOM	591	NZ	LYS	278	26.214	7.801	2.259	1.00	28.08
ATOM	592	C	LYS	278	23.862	7.317	8.361	1.00	25.78
ATOM	593	O	LYS	278	23.866	6.091	8.271	1.00	26.96
ATOM	594	N	ARG	279	24.388	7.950	9.400	1.00	26.39
ATOM	595	CA	ARG	279	24.999	7.195	10.482	1.00	27.59
ATOM	596	CB	ARG	279	26.266	7.893	10.953	1.00	28.22
ATOM	597	CG	ARG	279	27.190	8.219	9.794	1.00	31.75
ATOM	598	CD	ARG	279	28.645	8.302	10.202	1.00	33.61
ATOM	599	NE	ARG	279	29.490	8.575	9.047	1.00	35.68
ATOM	600	CZ	ARG	279	30.818	8.479	9.035	1.00	38.22
ATOM	601	NH1	ARG	279	31.478	8.108	10.128	1.00	38.46
ATOM	602	NH2	ARG	279	31.488	8.760	7.920	1.00	37.61
ATOM	603	C	ARG	279	24.053	6.936	11.652	1.00	27.34
ATOM	604	O	ARG	279	24.397	6.217	12.589	1.00	28.95
ATOM	605	N	ILE	280	22.854	7.503	11.596	1.00	25.28
ATOM	606	CA	ILE	280	21.886	7.270	12.661	1.00	24.59
ATOM	607	CB	ILE	280	20.922	8.464	12.827	1.00	22.88
ATOM	608	CG2	ILE	280	19.884	8.152	13.912	1.00	21.69
ATOM	609	CG1	ILE	280	21.708	9.722	13.219	1.00	21.57
ATOM	610	CD1	ILE	280	20.835	10.965	13.380	1.00	20.98
ATOM	611	C	ILE	280	21.085	6.014	12.315	1.00	24.77
ATOM	612	O	ILE	280	20.181	6.051	11.481	1.00	23.84
ATOM	613	N	THR	281	21.421	4.902	12.967	1.00	25.98
ATOM	614	CA	THR	281	20.754	3.628	12.706	1.00	27.40
ATOM	615	CB	THR	281	21.064	2.608	13.805	1.00	28.22
ATOM	616	OG1	THR	281	22.485	2.514	13.970	1.00	32.17
ATOM	617	CG2	THR	281	20.518	1.237	13.422	1.00	30.45
ATOM	618	C	THR	281	19.236	3.720	12.547	1.00	26.89
ATOM	619	O	THR	281	18.685	3.173	11.596	1.00	27.85
ATOM	620	N	GLY	282	18.568	4.405	13.468	1.00	25.97
ATOM	621	CA	GLY	282	17.120	4.536	13.395	1.00	24.93
ATOM	622	C	GLY	282	16.605	5.255	12.156	1.00	25.15
ATOM	623	O	GLY	282	15.502	4.981	11.680	1.00	23.70
ATOM	624	N	PHE	283	17.400	6.187	11.639	1.00	24.97
ATOM	625	CA	PHE	283	17.035	6.948	10.439	1.00	25.33
ATOM	626	CB	PHE	283	17.958	8.169	10.295	1.00	23.28
ATOM	627	CG	PHE	283	17.757	8.945	9.017	1.00	23.75
ATOM	628	CD1	PHE	283	18.377	8.548	7.837	1.00	23.86
ATOM	629	CD2	PHE	283	16.940	10.069	8.994	1.00	22.16
ATOM	630	CE1	PHE	283	18.185	9.261	6.654	1.00	23.03

ATOM	631	CE2	PHE	283	16.743	10.784	7.820	1.00	23.21
ATOM	632	CZ	PHE	283	17.367	10.382	6.648	1.00	20.80
ATOM	633	C	PHE	283	17.141	6.072	9.185	1.00	25.72
ATOM	634	O	PHE	283	16.287	6.128	8.295	1.00	26.38
ATOM	635	N	MET	284	18.194	5.265	9.115	1.00	26.64
ATOM	636	CA	MET	284	18.384	4.398	7.960	1.00	28.17
ATOM	637	CB	MET	284	19.825	3.887	7.916	1.00	29.11
ATOM	638	CG	MET	284	20.836	4.994	7.618	1.00	30.38
ATOM	639	SD	MET	284	20.370	6.064	6.205	1.00	33.12
ATOM	640	CE	MET	284	20.937	5.078	4.772	1.00	34.35
ATOM	641	C	MET	284	17.395	3.235	7.917	1.00	29.78
ATOM	642	O	MET	284	17.313	2.516	6.917	1.00	28.85
ATOM	643	N	GLU	285	16.629	3.068	8.991	1.00	31.01
ATOM	644	CA	GLU	285	15.638	1.999	9.060	1.00	31.97
ATOM	645	CB	GLU	285	15.439	1.536	10.507	1.00	33.56
ATOM	646	CG	GLU	285	16.658	0.814	11.078	1.00	37.02
ATOM	647	CD	GLU	285	16.417	0.259	12.469	1.00	38.77
ATOM	648	OE1	GLU	285	15.390	0.617	13.090	1.00	39.52
ATOM	649	OE2	GLU	285	17.265	-0.529	12.942	1.00	40.58
ATOM	650	C	GLU	285	14.306	2.444	8.479	1.00	31.93
ATOM	651	O	GLU	285	13.430	1.619	8.211	1.00	32.23
ATOM	652	N	LEU	286	14.153	3.754	8.289	1.00	30.77
ATOM	653	CA	LEU	286	12.935	4.315	7.715	1.00	30.76
ATOM	654	CB	LEU	286	12.890	5.835	7.931	1.00	29.72
ATOM	655	CG	LEU	286	13.009	6.367	9.364	1.00	29.96
ATOM	656	CD1	LEU	286	12.937	7.884	9.339	1.00	28.70
ATOM	657	CD2	LEU	286	11.890	5.805	10.235	1.00	29.71
ATOM	658	C	LEU	286	12.960	4.011	6.220	1.00	29.96
ATOM	659	O	LEU	286	14.021	3.715	5.666	1.00	30.54
ATOM	660	N	CYS	287	11.814	4.075	5.555	1.00	30.89
ATOM	661	CA	CYS	287	11.821	3.791	4.123	1.00	31.57
ATOM	662	CB	CYS	287	10.400	3.677	3.555	1.00	32.51
ATOM	663	SG	CYS	287	9.395	5.168	3.569	1.00	35.47
ATOM	664	C	CYS	287	12.579	4.921	3.457	1.00	31.76
ATOM	665	O	CYS	287	12.504	6.071	3.891	1.00	30.50
ATOM	666	N	GLN	288	13.327	4.591	2.411	1.00	32.56
ATOM	667	CA	GLN	288	14.134	5.591	1.723	1.00	32.18
ATOM	668	CB	GLN	288	14.818	4.960	0.519	1.00	34.37
ATOM	669	CG	GLN	288	16.070	5.697	0.077	1.00	37.44
ATOM	670	CD	GLN	288	16.766	4.982	-1.045	1.00	38.80
ATOM	671	OE1	GLN	288	16.178	4.741	-2.095	1.00	40.25
ATOM	672	NE2	GLN	288	18.023	4.626	-0.832	1.00	41.12
ATOM	673	C	GLN	288	13.304	6.800	1.305	1.00	31.30
ATOM	674	O	GLN	288	13.809	7.918	1.213	1.00	29.76
ATOM	675	N	ASN	289	12.019	6.586	1.063	1.00	29.60
ATOM	676	CA	ASN	289	11.180	7.701	0.685	1.00	30.09
ATOM	677	CB	ASN	289	9.789	7.222	0.320	1.00	32.43
ATOM	678	CG	ASN	289	8.831	8.363	0.186	1.00	34.94
ATOM	679	OD1	ASN	289	8.262	8.837	1.177	1.00	37.17
ATOM	680	ND2	ASN	289	8.670	8.850	-1.038	1.00	37.46
ATOM	681	C	ASN	289	11.065	8.737	1.803	1.00	28.55
ATOM	682	O	ASN	289	11.120	9.954	1.561	1.00	28.23
ATOM	683	N	ASP	290	10.880	8.253	3.027	1.00	27.44
ATOM	684	CA	ASP	290	10.759	9.146	4.166	1.00	25.42
ATOM	685	CB	ASP	290	10.100	8.423	5.351	1.00	25.58
ATOM	686	CG	ASP	290	8.593	8.245	5.159	1.00	25.63
ATOM	687	OD1	ASP	290	8.033	8.887	4.247	1.00	25.74
ATOM	688	OD2	ASP	290	7.966	7.479	5.918	1.00	24.50
ATOM	689	C	ASP	290	12.116	9.712	4.541	1.00	24.26
ATOM	690	O	ASP	290	12.205	10.793	5.113	1.00	23.09
ATOM	691	N	GLN	291	13.176	8.984	4.203	1.00	24.37
ATOM	692	CA	GLN	291	14.525	9.453	4.482	1.00	23.42
ATOM	693	CB	GLN	291	15.562	8.400	4.092	1.00	23.59
ATOM	694	CG	GLN	291	15.608	7.164	4.965	1.00	22.66
ATOM	695	CD	GLN	291	16.639	6.173	4.464	1.00	22.68
ATOM	696	OE1	GLN	291	17.532	6.527	3.694	1.00	24.72
ATOM	697	NE2	GLN	291	16.532	4.930	4.908	1.00	24.25
ATOM	698	C	GLN	291	14.773	10.704	3.649	1.00	23.72
ATOM	699	O	GLN	291	15.328	11.688	4.134	1.00	21.67
ATOM	700	N	ILE	292	14.358	10.648	2.384	1.00	23.54
ATOM	701	CA	ILE	292	14.541	11.765	1.462	1.00	23.40
ATOM	702	CB	ILE	292	14.166	11.363	-0.003	1.00	24.40
ATOM	703	CG2	ILE	292	14.176	12.592	-0.913	1.00	24.00
ATOM	704	CG1	ILE	292	15.160	10.326	-0.535	1.00	25.84
ATOM	705	CD1	ILE	292	16.582	10.825	-0.654	1.00	28.34
ATOM	706	C	ILE	292	13.681	12.938	1.903	1.00	22.88
ATOM	707	O	ILE	292	14.148	14.078	1.952	1.00	22.08
ATOM	708	N	LEU	293	12.430	12.649	2.245	1.00	21.21
ATOM	709	CA	LEU	293	11.513	13.679	2.684	1.00	22.20
ATOM	710	CB	LEU	293	10.128	13.077	2.945	1.00	22.87
ATOM	711	CG	LEU	293	9.337	12.783	1.668	1.00	26.65
ATOM	712	CD1	LEU	293	8.100	11.943	1.981	1.00	27.63
ATOM	713	CD2	LEU	293	8.947	14.115	1.009	1.00	27.30
ATOM	714	C	LEU	293	12.041	14.366	3.936	1.00	21.47
ATOM	715	O	LEU	293	12.013	15.588	4.034	1.00	20.74
ATOM	716	N	LEU	294	12.532	13.578	4.887	1.00	22.09

ATOM	717	CA	LEU	294	13.053	14.158	6.111	1.00	21.85
ATOM	718	CB	LEU	294	13.410	13.062	7.120	1.00	22.49
ATOM	719	CG	LEU	294	12.210	12.367	7.770	1.00	23.61
ATOM	720	CD1	LEU	294	12.693	11.448	8.877	1.00	23.93
ATOM	721	CD2	LEU	294	11.254	13.400	8.339	1.00	23.56
ATOM	722	C	LEU	294	14.262	15.034	5.818	1.00	20.92
ATOM	723	O	LEU	294	14.371	16.138	6.335	1.00	20.70
ATOM	724	N	LEU	295	15.170	14.549	4.979	1.00	21.44
ATOM	725	CA	LEU	295	16.352	15.334	4.636	1.00	21.46
ATOM	726	CB	LEU	295	17.325	14.481	3.836	1.00	21.73
ATOM	727	CG	LEU	295	18.087	13.499	4.725	1.00	24.02
ATOM	728	CD1	LEU	295	18.824	12.477	3.879	1.00	23.40
ATOM	729	CD2	LEU	295	19.053	14.292	5.602	1.00	25.66
ATOM	730	C	LEU	295	16.020	16.605	3.857	1.00	21.70
ATOM	731	O	LEU	295	16.537	17.682	4.158	1.00	19.82
ATOM	732	N	LYS	296	15.158	16.473	2.855	1.00	21.79
ATOM	733	CA	LYS	296	14.769	17.605	2.029	1.00	25.11
ATOM	734	CB	LYS	296	13.821	17.139	0.919	1.00	27.17
ATOM	735	CG	LYS	296	13.241	18.257	0.084	1.00	30.32
ATOM	736	CD	LYS	296	12.261	17.694	-0.938	1.00	33.40
ATOM	737	CE	LYS	296	11.800	18.766	-1.903	1.00	35.42
ATOM	738	NZ	LYS	296	12.910	19.218	-2.791	1.00	37.44
ATOM	739	C	LYS	296	14.109	18.714	2.831	1.00	23.87
ATOM	740	O	LYS	296	14.348	19.902	2.582	1.00	23.29
ATOM	741	N	SER	297	13.287	18.326	3.798	1.00	23.52
ATOM	742	CA	SER	297	12.587	19.294	4.628	1.00	24.66
ATOM	743	CB	SER	297	11.243	18.707	5.086	1.00	25.85
ATOM	744	OG	SER	297	11.426	17.494	5.798	1.00	25.78
ATOM	745	C	SER	297	13.374	19.791	5.852	1.00	24.58
ATOM	746	O	SER	297	13.123	20.898	6.338	1.00	25.12
ATOM	747	N	GLY	298	14.333	19.002	6.328	1.00	22.15
ATOM	748	CA	GLY	298	15.068	19.406	7.511	1.00	22.02
ATOM	749	C	GLY	298	16.570	19.616	7.445	1.00	20.47
ATOM	750	O	GLY	298	17.160	20.017	8.437	1.00	20.04
ATOM	751	N	CYS	299	17.203	19.363	6.306	1.00	20.94
ATOM	752	CA	CYS	299	18.649	19.543	6.237	1.00	21.39
ATOM	753	CB	CYS	299	19.182	19.250	4.827	1.00	23.06
ATOM	754	SG	CYS	299	18.429	20.203	3.482	1.00	29.00
ATOM	755	C	CYS	299	19.039	20.951	6.658	1.00	20.07
ATOM	756	O	CYS	299	19.907	21.121	7.506	1.00	18.32
ATOM	757	N	LEU	300	18.379	21.958	6.097	1.00	18.43
ATOM	758	CA	LEU	300	18.704	23.335	6.443	1.00	18.89
ATOM	759	CB	LEU	300	17.942	24.303	5.540	1.00	17.66
ATOM	760	CG	LEU	300	18.466	25.744	5.496	1.00	18.57
ATOM	761	CD1	LEU	300	19.961	25.753	5.152	1.00	18.04
ATOM	762	CD2	LEU	300	17.670	26.535	4.469	1.00	18.71
ATOM	763	C	LEU	300	18.424	23.657	7.913	1.00	18.49
ATOM	764	O	LEU	300	19.151	24.435	8.535	1.00	18.49
ATOM	765	N	GLU	301	17.368	23.061	8.462	1.00	18.69
ATOM	766	CA	GLU	301	17.020	23.278	9.858	1.00	18.42
ATOM	767	CB	GLU	301	15.680	22.604	10.181	1.00	18.90
ATOM	768	CG	GLU	301	14.505	23.235	9.443	1.00	21.00
ATOM	769	CD	GLU	301	13.163	22.710	9.897	1.00	22.11
ATOM	770	OE1	GLU	301	13.145	21.861	10.809	1.00	22.99
ATOM	771	OE2	GLU	301	12.128	23.156	9.342	1.00	23.74
ATOM	772	C	GLU	301	18.137	22.729	10.744	1.00	18.45
ATOM	773	O	GLU	301	18.488	23.327	11.764	1.00	17.98
ATOM	774	N	VAL	302	18.705	21.594	10.354	1.00	18.55
ATOM	775	CA	VAL	302	19.804	21.013	11.126	1.00	18.30
ATOM	776	CB	VAL	302	20.165	19.597	10.631	1.00	17.49
ATOM	777	CG1	VAL	302	21.417	19.094	11.337	1.00	17.23
ATOM	778	CG2	VAL	302	19.003	18.660	10.888	1.00	18.62
ATOM	779	C	VAL	302	21.037	21.913	10.991	1.00	18.44
ATOM	780	O	VAL	302	21.762	22.142	11.959	1.00	18.67
ATOM	781	N	VAL	303	21.274	22.413	9.782	1.00	17.76
ATOM	782	CA	VAL	303	22.406	23.296	9.546	1.00	17.41
ATOM	783	CB	VAL	303	22.461	23.762	8.074	1.00	17.57
ATOM	784	CG1	VAL	303	23.544	24.829	7.906	1.00	16.57
ATOM	785	CG2	VAL	303	22.737	22.574	7.156	1.00	18.12
ATOM	786	C	VAL	303	22.260	24.528	10.435	1.00	18.40
ATOM	787	O	VAL	303	23.219	24.985	11.051	1.00	18.46
ATOM	788	N	LEU	304	21.043	25.057	10.495	1.00	17.81
ATOM	789	CA	LEU	304	20.771	26.237	11.296	1.00	18.40
ATOM	790	CB	LEU	304	19.310	26.664	11.145	1.00	18.67
ATOM	791	CG	LEU	304	18.905	27.901	11.954	1.00	18.74
ATOM	792	CD1	LEU	304	19.798	29.072	11.572	1.00	19.24
ATOM	793	CD2	LEU	304	17.439	28.224	11.690	1.00	19.46
ATOM	794	C	LEU	304	21.089	25.994	12.762	1.00	19.34
ATOM	795	O	LEU	304	21.642	26.873	13.422	1.00	18.80
ATOM	796	N	VAL	305	20.720	24.811	13.265	1.00	19.25
ATOM	797	CA	VAL	305	20.984	24.439	14.655	1.00	19.61
ATOM	798	CB	VAL	305	20.342	23.072	15.031	1.00	20.39
ATOM	799	CG1	VAL	305	20.877	22.596	16.381	1.00	18.01
ATOM	800	CG2	VAL	305	18.819	23.192	15.081	1.00	18.19
ATOM	801	C	VAL	305	22.495	24.320	14.828	1.00	20.18
ATOM	802	O	VAL	305	23.059	24.849	15.779	1.00	20.30

ATOM	803	N	ARG	306	23.142	23.628	13.896	1.00	19.99
ATOM	804	CA	ARG	306	24.587	23.456	13.957	1.00	21.89
ATOM	805	CB	ARG	306	25.063	22.541	12.836	1.00	21.78
ATOM	806	CG	ARG	306	24.838	21.076	13.112	1.00	19.29
ATOM	807	CD	ARG	306	25.401	20.245	11.990	1.00	20.34
ATOM	808	NE	ARG	306	25.516	18.853	12.393	1.00	22.00
ATOM	809	CZ	ARG	306	26.166	17.928	11.702	1.00	22.25
ATOM	810	NH1	ARG	306	26.760	18.247	10.558	1.00	20.55
ATOM	811	NH2	ARG	306	26.241	16.692	12.173	1.00	22.86
ATOM	812	C	ARG	306	25.373	24.763	13.908	1.00	22.45
ATOM	813	O	ARG	306	26.474	24.840	14.445	1.00	22.73
ATOM	814	N	MET	307	24.805	25.785	13.277	1.00	24.18
ATOM	815	CA	MET	307	25.470	27.084	13.169	1.00	26.27
ATOM	816	CB	MET	307	24.608	28.046	12.353	1.00	27.38
ATOM	817	CG	MET	307	25.231	29.412	12.170	1.00	28.81
ATOM	818	SD	MET	307	24.099	30.460	11.288	1.00	30.68
ATOM	819	CE	MET	307	23.147	31.073	12.604	1.00	27.74
ATOM	820	C	MET	307	25.763	27.708	14.532	1.00	25.58
ATOM	821	O	MET	307	26.731	28.453	14.701	1.00	25.50
ATOM	822	N	CYS	308	24.921	27.400	15.505	1.00	26.62
ATOM	823	CA	CYS	308	25.087	27.935	16.842	1.00	25.94
ATOM	824	CB	CYS	308	23.901	27.512	17.693	1.00	27.50
ATOM	825	SG	CYS	308	22.349	27.999	16.879	1.00	32.50
ATOM	826	C	CYS	308	26.411	27.483	17.451	1.00	25.08
ATOM	827	O	CYS	308	26.951	28.139	18.337	1.00	26.40
ATOM	828	N	ARG	309	26.932	26.367	16.958	1.00	24.15
ATOM	829	CA	ARG	309	28.212	25.836	17.426	1.00	23.77
ATOM	830	CB	ARG	309	28.514	24.490	16.763	1.00	22.37
ATOM	831	CG	ARG	309	27.526	23.377	17.070	1.00	23.29
ATOM	832	CD	ARG	309	27.900	22.123	16.296	1.00	22.66
ATOM	833	NE	ARG	309	29.133	21.499	16.778	1.00	23.68
ATOM	834	CZ	ARG	309	30.260	21.397	16.079	1.00	22.00
ATOM	835	NH1	ARG	309	30.337	21.884	14.850	1.00	20.45
ATOM	836	NH2	ARG	309	31.309	20.777	16.612	1.00	21.98
ATOM	837	C	ARG	309	29.337	26.792	17.043	1.00	23.79
ATOM	838	O	ARG	309	30.334	26.918	17.758	1.00	23.81
ATOM	839	N	ALA	310	29.167	27.438	15.892	1.00	23.32
ATOM	840	CA	ALA	310	30.167	28.354	15.344	1.00	22.67
ATOM	841	CB	ALA	310	30.501	27.953	13.903	1.00	23.22
ATOM	842	C	ALA	310	29.690	29.796	15.376	1.00	22.59
ATOM	843	O	ALA	310	29.895	30.549	14.424	1.00	22.73
ATOM	844	N	PHE	311	29.047	30.170	16.471	1.00	22.48
ATOM	845	CA	PHE	311	28.552	31.524	16.639	1.00	23.10
ATOM	846	CB	PHE	311	27.025	31.516	16.677	1.00	22.61
ATOM	847	CG	PHE	311	26.419	32.879	16.811	1.00	24.45
ATOM	848	CD1	PHE	311	26.166	33.422	18.066	1.00	25.03
ATOM	849	CD2	PHE	311	26.111	33.625	15.677	1.00	24.86
ATOM	850	CE1	PHE	311	25.610	34.697	18.189	1.00	26.19
ATOM	851	CE2	PHE	311	25.555	34.904	15.787	1.00	25.65
ATOM	852	CZ	PHE	311	25.303	35.440	17.044	1.00	25.80
ATOM	853	C	PHE	311	29.118	32.064	17.950	1.00	23.95
ATOM	854	O	PHE	311	29.225	31.332	18.926	1.00	24.13
ATOM	855	N	ASN	312	29.496	33.336	17.965	1.00	23.37
ATOM	856	CA	ASN	312	30.041	33.928	19.170	1.00	23.53
ATOM	857	CB	ASN	312	31.413	34.524	18.884	1.00	24.46
ATOM	858	CG	ASN	312	32.066	35.059	20.125	1.00	25.90
ATOM	859	OD1	ASN	312	31.439	35.112	21.187	1.00	28.29
ATOM	860	ND2	ASN	312	33.326	35.465	20.009	1.00	25.97
ATOM	861	C	ASN	312	29.091	35.015	19.670	1.00	23.70
ATOM	862	O	ASN	312	29.051	36.121	19.127	1.00	22.70
ATOM	863	N	PRO	313	28.309	34.707	20.715	1.00	23.93
ATOM	864	CD	PRO	313	28.291	33.413	21.415	1.00	24.49
ATOM	865	CA	PRO	313	27.340	35.635	21.307	1.00	25.73
ATOM	866	CB	PRO	313	26.561	34.748	22.283	1.00	25.50
ATOM	867	CG	PRO	313	27.557	33.738	22.691	1.00	25.23
ATOM	868	C	PRO	313	27.955	36.856	21.976	1.00	26.34
ATOM	869	O	PRO	313	27.271	37.852	22.209	1.00	27.02
ATOM	870	N	LEU	314	29.243	36.782	22.283	1.00	27.08
ATOM	871	CA	LEU	314	29.933	37.908	22.900	1.00	28.42
ATOM	872	CB	LEU	314	31.384	37.525	23.202	1.00	29.58
ATOM	873	CG	LEU	314	31.588	36.580	24.390	1.00	30.01
ATOM	874	CD1	LEU	314	32.985	35.966	24.353	1.00	30.50
ATOM	875	CD2	LEU	314	31.366	37.344	25.685	1.00	31.31
ATOM	876	C	LEU	314	29.881	39.134	21.980	1.00	29.42
ATOM	877	O	LEU	314	29.618	40.247	22.438	1.00	29.09
ATOM	878	N	ASN	315	30.119	38.918	20.685	1.00	28.55
ATOM	879	CA	ASN	315	30.104	39.995	19.699	1.00	28.31
ATOM	880	CB	ASN	315	31.520	40.220	19.135	1.00	28.09
ATOM	881	CG	ASN	315	32.114	38.966	18.488	1.00	28.61
ATOM	882	OD1	ASN	315	31.459	37.935	18.375	1.00	27.11
ATOM	883	ND2	ASN	315	33.368	39.065	18.053	1.00	29.33
ATOM	884	C	ASN	315	29.123	39.771	18.536	1.00	28.16
ATOM	885	O	ASN	315	29.115	40.534	17.566	1.00	28.31
ATOM	886	N	ASN	316	28.289	38.742	18.637	1.00	27.03
ATOM	887	CA	ASN	316	27.322	38.430	17.582	1.00	26.93
ATOM	888	CB	ASN	316	26.246	39.522	17.467	1.00	27.40

ATOM	889	CG	ASN	316	25.247	39.491	18.621	1.00	29.23
ATOM	890	OD1	ASN	316	24.845	38.423	19.079	1.00	29.19
ATOM	891	ND2	ASN	316	24.828	40.673	19.081	1.00	29.80
ATOM	892	C	ASN	316	28.002	38.253	16.226	1.00	25.60
ATOM	893	O	ASN	316	27.688	38.956	15.264	1.00	25.51
ATOM	894	N	THR	317	28.947	37.322	16.162	1.00	24.54
ATOM	895	CA	THR	317	29.635	37.031	14.917	1.00	24.24
ATOM	896	CB	THR	317	31.124	37.428	14.970	1.00	24.58
ATOM	897	OG1	THR	317	31.780	36.721	16.029	1.00	25.19
ATOM	898	CG2	THR	317	31.255	38.924	15.194	1.00	24.84
ATOM	899	C	THR	317	29.516	35.532	14.648	1.00	22.99
ATOM	900	O	THR	317	29.262	34.741	15.559	1.00	22.92
ATOM	901	N	VAL	318	29.674	35.154	13.388	1.00	22.45
ATOM	902	CA	VAL	318	29.577	33.761	13.004	1.00	22.06
ATOM	903	CB	VAL	318	28.239	33.460	12.281	1.00	21.83
ATOM	904	CG1	VAL	318	28.127	34.294	11.017	1.00	21.77
ATOM	905	CG2	VAL	318	28.155	31.983	11.950	1.00	23.58
ATOM	906	C	VAL	318	30.719	33.402	12.081	1.00	21.76
ATOM	907	O	VAL	318	31.245	34.256	11.366	1.00	21.99
ATOM	908	N	LEU	319	31.109	32.132	12.122	1.00	21.37
ATOM	909	CA	LEU	319	32.177	31.626	11.278	1.00	22.24
ATOM	910	CB	LEU	319	32.619	30.243	11.767	1.00	22.86
ATOM	911	CG	LEU	319	33.660	29.513	10.921	1.00	23.05
ATOM	912	CD1	LEU	319	34.955	30.318	10.928	1.00	25.19
ATOM	913	CD2	LEU	319	33.896	28.116	11.475	1.00	24.34
ATOM	914	C	LEU	319	31.684	31.528	9.833	1.00	23.30
ATOM	915	O	LEU	319	30.687	30.870	9.551	1.00	22.87
ATOM	916	N	PHE	320	32.389	32.194	8.925	1.00	23.64
ATOM	917	CA	PHE	320	32.037	32.176	7.508	1.00	25.23
ATOM	918	CB	PHE	320	31.108	33.346	7.172	1.00	24.27
ATOM	919	CG	PHE	320	30.699	33.397	5.729	1.00	25.29
ATOM	920	CD1	PHE	320	29.735	32.522	5.229	1.00	25.59
ATOM	921	CD2	PHE	320	31.269	34.325	4.865	1.00	24.72
ATOM	922	CE1	PHE	320	29.347	32.576	3.894	1.00	25.95
ATOM	923	CE2	PHE	320	30.886	34.383	3.525	1.00	25.91
ATOM	924	CZ	PHE	320	29.924	33.509	3.040	1.00	25.81
ATOM	925	C	PHE	320	33.327	32.290	6.702	1.00	26.25
ATOM	926	O	PHE	320	34.045	33.284	6.787	1.00	26.22
ATOM	927	N	GLU	321	33.621	31.255	5.929	1.00	28.45
ATOM	928	CA	GLU	321	34.831	31.210	5.125	1.00	29.34
ATOM	929	CB	GLU	321	34.779	32.272	4.006	1.00	29.96
ATOM	930	CG	GLU	321	33.650	32.017	2.999	1.00	31.85
ATOM	931	CD	GLU	321	33.659	32.933	1.774	1.00	32.92
ATOM	932	OE1	GLU	321	34.446	33.910	1.724	1.00	35.63
ATOM	933	OE2	GLU	321	32.860	32.667	0.855	1.00	31.62
ATOM	934	C	GLU	321	36.114	31.357	5.953	1.00	29.82
ATOM	935	O	GLU	321	36.994	32.128	5.602	1.00	29.97
ATOM	936	N	GLY	322	36.202	30.635	7.067	1.00	29.47
ATOM	937	CA	GLY	322	37.411	30.658	7.880	1.00	28.49
ATOM	938	C	GLY	322	37.607	31.596	9.062	1.00	27.90
ATOM	939	O	GLY	322	38.501	31.362	9.882	1.00	28.38
ATOM	940	N	LYS	323	36.824	32.663	9.160	1.00	26.69
ATOM	941	CA	LYS	323	36.979	33.591	10.280	1.00	26.84
ATOM	942	CB	LYS	323	37.836	34.801	9.878	1.00	28.64
ATOM	943	CG	LYS	323	39.232	34.483	9.329	1.00	31.90
ATOM	944	CD	LYS	323	39.949	35.778	8.935	1.00	34.33
ATOM	945	CE	LYS	323	41.320	35.534	8.325	1.00	36.36
ATOM	946	NZ	LYS	323	42.359	35.109	9.323	1.00	38.14
ATOM	947	C	LYS	323	35.608	34.087	10.707	1.00	25.87
ATOM	948	O	LYS	323	34.638	33.952	9.961	1.00	23.69
ATOM	949	N	TYR	324	35.526	34.672	11.899	1.00	25.68
ATOM	950	CA	TYR	324	34.249	35.186	12.378	1.00	25.45
ATOM	951	CB	TYR	324	34.205	35.174	13.903	1.00	26.32
ATOM	952	CG	TYR	324	33.996	33.794	14.474	1.00	26.94
ATOM	953	CD1	TYR	324	34.918	32.773	14.237	1.00	27.29
ATOM	954	CE1	TYR	324	34.705	31.486	14.722	1.00	28.49
ATOM	955	CD2	TYR	324	32.858	33.491	15.215	1.00	25.92
ATOM	956	CE2	TYR	324	32.640	32.210	15.702	1.00	26.59
ATOM	957	CZ	TYR	324	33.564	31.211	15.451	1.00	27.01
ATOM	958	OH	TYR	324	33.339	29.930	15.920	1.00	28.62
ATOM	959	C	TYR	324	33.965	36.585	11.863	1.00	25.14
ATOM	960	O	TYR	324	34.864	37.422	11.781	1.00	25.62
ATOM	961	N	GLY	325	32.705	36.829	11.507	1.00	23.90
ATOM	962	CA	GLY	325	32.310	38.127	11.001	1.00	23.79
ATOM	963	C	GLY	325	30.897	38.461	11.441	1.00	25.33
ATOM	964	O	GLY	325	30.079	37.561	11.652	1.00	24.38
ATOM	965	N	GLY	326	30.610	39.752	11.589	1.00	24.25
ATOM	966	CA	GLY	326	29.282	40.168	12.004	1.00	24.94
ATOM	967	C	GLY	326	28.261	40.090	10.883	1.00	25.23
ATOM	968	O	GLY	326	28.598	39.728	9.751	1.00	25.79
ATOM	969	N	MET	327	27.014	40.445	11.185	1.00	26.02
ATOM	970	CA	MET	327	25.953	40.401	10.190	1.00	27.32
ATOM	971	CB	MET	327	24.595	40.646	10.864	1.00	29.29
ATOM	972	CG	MET	327	24.389	42.052	11.416	1.00	32.37
ATOM	973	SD	MET	327	23.965	43.257	10.146	1.00	37.07
ATOM	974	CE	MET	327	22.345	42.637	9.596	1.00	35.38

ATOM	975	C	MET	327	26.152	41.373	9.017	1.00	27.13
ATOM	976	O	MET	327	25.592	41.172	7.950	1.00	25.51
ATOM	977	N	GLN	328	26.950	42.423	9.211	1.00	27.79
ATOM	978	CA	GLN	328	27.198	43.392	8.138	1.00	29.04
ATOM	979	CB	GLN	328	28.025	44.571	8.662	1.00	31.55
ATOM	980	CG	GLN	328	29.460	44.204	8.990	1.00	33.92
ATOM	981	CD	GLN	328	29.682	43.901	10.462	1.00	36.11
ATOM	982	OE1	GLN	328	28.873	43.216	11.102	1.00	35.48
ATOM	983	NE2	GLN	328	30.802	44.407	11.011	1.00	36.91
ATOM	984	C	GLN	328	27.959	42.718	6.993	1.00	28.92
ATOM	985	O	GLN	328	27.970	43.193	5.864	1.00	28.52
ATOM	986	N	MET	329	28.604	41.604	7.317	1.00	28.72
ATOM	987	CA	MET	329	29.368	40.813	6.366	1.00	27.66
ATOM	988	CB	MET	329	29.998	39.633	7.124	1.00	29.67
ATOM	989	CG	MET	329	30.698	38.584	6.294	1.00	30.31
ATOM	990	SD	MET	329	31.675	37.438	7.333	1.00	30.76
ATOM	991	CE	MET	329	30.395	36.763	8.395	1.00	27.38
ATOM	992	C	MET	329	28.462	40.322	5.228	1.00	27.08
ATOM	993	O	MET	329	28.927	40.093	4.115	1.00	25.67
ATOM	994	N	PHE	330	27.166	40.197	5.505	1.00	25.56
ATOM	995	CA	PHE	330	26.202	39.717	4.510	1.00	25.27
ATOM	996	CB	PHE	330	25.258	38.717	5.164	1.00	26.21
ATOM	997	CG	PHE	330	25.960	37.546	5.779	1.00	26.31
ATOM	998	CD1	PHE	330	26.573	36.591	4.979	1.00	26.75
ATOM	999	CD2	PHE	330	26.037	37.413	7.160	1.00	27.20
ATOM	1000	CE1	PHE	330	27.263	35.514	5.547	1.00	28.46
ATOM	1001	CE2	PHE	330	26.722	36.342	7.737	1.00	28.83
ATOM	1002	CZ	PHE	330	27.337	35.391	6.928	1.00	27.19
ATOM	1003	C	PHE	330	25.368	40.812	3.858	1.00	24.89
ATOM	1004	O	PHE	330	24.351	40.536	3.226	1.00	24.95
ATOM	1005	N	LYS	331	25.803	42.051	4.007	1.00	24.84
ATOM	1006	CA	LYS	331	25.081	43.181	3.452	1.00	25.68
ATOM	1007	CB	LYS	331	25.923	44.442	3.602	1.00	27.69
ATOM	1008	CG	LYS	331	25.100	45.699	3.629	1.00	30.20
ATOM	1009	CD	LYS	331	24.105	45.611	4.781	1.00	34.11
ATOM	1010	CE	LYS	331	23.238	46.853	4.879	1.00	35.87
ATOM	1011	NZ	LYS	331	22.167	46.684	5.903	1.00	37.65
ATOM	1012	C	LYS	331	24.679	43.007	1.990	1.00	26.00
ATOM	1013	O	LYS	331	23.551	43.317	1.609	1.00	26.68
ATOM	1014	N	ALA	332	25.594	42.493	1.182	1.00	26.27
ATOM	1015	CA	ALA	332	25.357	42.299	-0.242	1.00	26.94
ATOM	1016	CB	ALA	332	26.645	41.847	-0.917	1.00	27.13
ATOM	1017	C	ALA	332	24.211	41.348	-0.588	1.00	27.68
ATOM	1018	O	ALA	332	23.687	41.398	-1.705	1.00	28.00
ATOM	1019	N	LEU	333	23.817	40.492	0.356	1.00	26.04
ATOM	1020	CA	LEU	333	22.709	39.566	0.119	1.00	25.55
ATOM	1021	CB	LEU	333	22.548	38.586	1.279	1.00	22.80
ATOM	1022	CG	LEU	333	23.589	37.495	1.501	1.00	23.44
ATOM	1023	CD1	LEU	333	23.127	36.616	2.659	1.00	21.98
ATOM	1024	CD2	LEU	333	23.766	36.673	0.241	1.00	24.51
ATOM	1025	C	LEU	333	21.391	40.318	-0.048	1.00	25.80
ATOM	1026	O	LEU	333	20.454	39.807	-0.644	1.00	26.35
ATOM	1027	N	GLY	334	21.330	41.533	0.480	1.00	26.06
ATOM	1028	CA	GLY	334	20.115	42.307	0.387	1.00	27.61
ATOM	1029	C	GLY	334	18.980	41.627	1.127	1.00	28.38
ATOM	1030	O	GLY	334	17.821	41.762	0.743	1.00	29.21
ATOM	1031	N	SER	335	19.313	40.898	2.191	1.00	28.07
ATOM	1032	CA	SER	335	18.310	40.190	2.984	1.00	28.11
ATOM	1033	CB	SER	335	18.251	38.723	2.551	1.00	29.24
ATOM	1034	OG	SER	335	18.153	38.604	1.143	1.00	31.20
ATOM	1035	C	SER	335	18.648	40.266	4.474	1.00	28.25
ATOM	1036	O	SER	335	18.816	39.235	5.134	1.00	27.31
ATOM	1037	N	ASP	336	18.751	41.482	5.004	1.00	27.15
ATOM	1038	CA	ASP	336	19.080	41.661	6.411	1.00	27.95
ATOM	1039	CB	ASP	336	19.182	43.146	6.758	1.00	28.40
ATOM	1040	CG	ASP	336	20.462	43.776	6.256	1.00	31.17
ATOM	1041	OD1	ASP	336	21.300	43.061	5.671	1.00	30.76
ATOM	1042	OD2	ASP	336	20.630	45.000	6.450	1.00	33.65
ATOM	1043	C	ASP	336	18.054	41.000	7.321	1.00	27.32
ATOM	1044	O	ASP	336	18.393	40.523	8.406	1.00	27.74
ATOM	1045	N	ASP	337	16.799	40.985	6.887	1.00	26.73
ATOM	1046	CA	ASP	337	15.748	40.364	7.678	1.00	27.00
ATOM	1047	CB	ASP	337	14.383	40.532	6.982	1.00	29.56
ATOM	1048	CG	ASP	337	14.362	39.994	5.564	1.00	30.90
ATOM	1049	OD1	ASP	337	15.434	39.888	4.931	1.00	32.90
ATOM	1050	OD2	ASP	337	13.251	39.693	5.066	1.00	32.99
ATOM	1051	C	ASP	337	16.082	38.886	7.917	1.00	25.07
ATOM	1052	O	ASP	337	15.948	38.375	9.031	1.00	23.90
ATOM	1053	N	LEU	338	16.537	38.210	6.873	1.00	23.72
ATOM	1054	CA	LEU	338	16.904	36.809	6.997	1.00	23.15
ATOM	1055	CB	LEU	338	17.174	36.212	5.618	1.00	21.77
ATOM	1056	CG	LEU	338	17.719	34.783	5.629	1.00	22.22
ATOM	1057	CD1	LEU	338	16.705	33.837	6.276	1.00	22.75
ATOM	1058	CD2	LEU	338	18.021	34.355	4.206	1.00	20.63
ATOM	1059	C	LEU	338	18.144	36.668	7.880	1.00	22.07
ATOM	1060	O	LEU	338	18.176	35.856	8.799	1.00	22.27

ATOM	1061	N	VAL	339	19.165	37.474	7.610	1.00	22.77
ATOM	1062	CA	VAL	339	20.388	37.406	8.403	1.00	23.12
ATOM	1063	CB	VAL	339	21.448	38.408	7.893	1.00	23.99
ATOM	1064	CG1	VAL	339	22.718	38.275	8.717	1.00	23.37
ATOM	1065	CG2	VAL	339	21.732	38.163	6.411	1.00	24.06
ATOM	1066	C	VAL	339	20.108	37.690	9.884	1.00	23.24
ATOM	1067	O	VAL	339	20.611	36.998	10.770	1.00	22.39
ATOM	1068	N	ASN	340	19.296	38.708	10.150	1.00	24.30
ATOM	1069	CA	ASN	340	18.973	39.065	11.522	1.00	25.14
ATOM	1070	CB	ASN	340	18.205	40.391	11.561	1.00	28.38
ATOM	1071	CG	ASN	340	19.134	41.592	11.610	1.00	30.44
ATOM	1072	OD1	ASN	340	18.844	42.649	11.042	1.00	33.87
ATOM	1073	ND2	ASN	340	20.258	41.440	12.303	1.00	31.74
ATOM	1074	C	ASN	340	18.189	37.970	12.229	1.00	24.36
ATOM	1075	O	ASN	340	18.392	37.737	13.415	1.00	23.30
ATOM	1076	N	GLU	341	17.294	37.298	11.514	1.00	24.45
ATOM	1077	CA	GLU	341	16.527	36.224	12.139	1.00	24.75
ATOM	1078	CB	GLU	341	15.350	35.814	11.254	1.00	26.89
ATOM	1079	CG	GLU	341	14.179	36.773	11.358	1.00	31.50
ATOM	1080	CD	GLU	341	12.945	36.239	10.681	1.00	34.84
ATOM	1081	OE1	GLU	341	12.720	35.013	10.750	1.00	37.24
ATOM	1082	OE2	GLU	341	12.187	37.038	10.096	1.00	37.28
ATOM	1083	C	GLU	341	17.432	35.027	12.417	1.00	23.12
ATOM	1084	O	GLU	341	17.290	34.356	13.448	1.00	22.72
ATOM	1085	N	ALA	342	18.365	34.766	11.506	1.00	21.14
ATOM	1086	CA	ALA	342	19.304	33.664	11.684	1.00	20.58
ATOM	1087	CB	ALA	342	20.158	33.498	10.442	1.00	19.08
ATOM	1088	C	ALA	342	20.193	33.943	12.906	1.00	21.25
ATOM	1089	O	ALA	342	20.386	33.074	13.764	1.00	21.78
ATOM	1090	N	PHE	343	20.720	35.164	12.987	1.00	21.28
ATOM	1091	CA	PHE	343	21.581	35.548	14.105	1.00	23.79
ATOM	1092	CB	PHE	343	22.201	36.933	13.864	1.00	22.95
ATOM	1093	CG	PHE	343	23.487	36.906	13.083	1.00	22.10
ATOM	1094	CD1	PHE	343	23.540	36.348	11.814	1.00	21.63
ATOM	1095	CD2	PHE	343	24.644	37.480	13.607	1.00	22.10
ATOM	1096	CE1	PHE	343	24.724	36.366	11.079	1.00	22.66
ATOM	1097	CE2	PHE	343	25.831	37.503	12.880	1.00	20.80
ATOM	1098	CZ	PHE	343	25.871	36.945	11.614	1.00	21.73
ATOM	1099	C	PHE	343	20.820	35.563	15.437	1.00	24.28
ATOM	1100	O	PHE	343	21.348	35.143	16.466	1.00	25.24
ATOM	1101	N	ASP	344	19.581	36.042	15.422	1.00	25.30
ATOM	1102	CA	ASP	344	18.807	36.088	16.655	1.00	27.20
ATOM	1103	CB	ASP	344	17.453	36.754	16.425	1.00	30.33
ATOM	1104	CG	ASP	344	17.581	38.215	16.084	1.00	34.37
ATOM	1105	OD1	ASP	344	18.728	38.719	16.068	1.00	36.85
ATOM	1106	OD2	ASP	344	16.529	38.853	15.835	1.00	36.92
ATOM	1107	C	ASP	344	18.600	34.674	17.165	1.00	25.45
ATOM	1108	O	ASP	344	18.728	34.400	18.364	1.00	25.36
ATOM	1109	N	PHE	345	18.274	33.770	16.250	1.00	24.47
ATOM	1110	CA	PHE	345	18.072	32.393	16.647	1.00	23.12
ATOM	1111	CB	PHE	345	17.703	31.513	15.457	1.00	23.28
ATOM	1112	CG	PHE	345	17.733	30.058	15.784	1.00	22.38
ATOM	1113	CD1	PHE	345	16.777	29.512	16.633	1.00	22.93
ATOM	1114	CD2	PHE	345	18.773	29.250	15.329	1.00	22.45
ATOM	1115	CE1	PHE	345	16.856	28.183	17.036	1.00	21.83
ATOM	1116	CE2	PHE	345	18.861	27.919	15.724	1.00	22.15
ATOM	1117	CZ	PHE	345	17.901	27.385	16.582	1.00	23.05
ATOM	1118	C	PHE	345	19.333	31.825	17.281	1.00	22.93
ATOM	1119	O	PHE	345	19.286	31.241	18.360	1.00	22.27
ATOM	1120	N	ALA	346	20.459	31.982	16.592	1.00	23.57
ATOM	1121	CA	ALA	346	21.712	31.457	17.099	1.00	25.20
ATOM	1122	CB	ALA	346	22.839	31.734	16.127	1.00	26.42
ATOM	1123	C	ALA	346	22.038	32.040	18.459	1.00	27.60
ATOM	1124	O	ALA	346	22.459	31.314	19.349	1.00	25.96
ATOM	1125	N	LYS	347	21.843	33.348	18.620	1.00	28.41
ATOM	1126	CA	LYS	347	22.127	33.985	19.901	1.00	30.85
ATOM	1127	CB	LYS	347	21.838	35.485	19.841	1.00	32.36
ATOM	1128	CG	LYS	347	21.860	36.147	21.202	1.00	36.99
ATOM	1129	CD	LYS	347	21.431	37.613	21.140	1.00	39.60
ATOM	1130	CE	LYS	347	21.227	38.185	22.561	1.00	42.60
ATOM	1131	NZ	LYS	347	22.459	38.130	23.428	1.00	42.88
ATOM	1132	C	LYS	347	21.298	33.355	21.011	1.00	30.95
ATOM	1133	O	LYS	347	21.847	32.949	22.039	1.00	31.24
ATOM	1134	N	ASN	348	19.986	33.259	20.807	1.00	30.97
ATOM	1135	CA	ASN	348	19.121	32.676	21.826	1.00	32.18
ATOM	1136	CB	ASN	348	17.645	32.804	21.435	1.00	34.34
ATOM	1137	CG	ASN	348	17.173	34.246	21.450	1.00	38.72
ATOM	1138	OD1	ASN	348	17.656	35.057	22.247	1.00	40.24
ATOM	1139	ND2	ASN	348	16.222	34.579	20.574	1.00	39.22
ATOM	1140	C	ASN	348	19.457	31.227	22.149	1.00	30.79
ATOM	1141	O	ASN	348	19.442	30.838	23.316	1.00	30.95
ATOM	1142	N	LEU	349	19.776	30.425	21.138	1.00	29.90
ATOM	1143	CA	LEU	349	20.122	29.033	21.409	1.00	29.04
ATOM	1144	CB	LEU	349	20.298	28.238	20.108	1.00	29.41
ATOM	1145	CG	LEU	349	20.380	26.738	20.388	1.00	28.84
ATOM	1146	CD1	LEU	349	19.012	26.269	20.904	1.00	29.78

ATOM	1147	CD2	LEU	349	20.756	25.976	19.136	1.00	30.12
ATOM	1148	C	LEU	349	21.419	28.977	22.212	1.00	28.27
ATOM	1149	O	LEU	349	21.527	28.229	23.181	1.00	28.13
ATOM	1150	N	CYS	350	22.405	29.768	21.802	1.00	27.19
ATOM	1151	CA	CYS	350	23.683	29.804	22.498	1.00	27.50
ATOM	1152	CB	CYS	350	24.618	30.856	21.875	1.00	27.40
ATOM	1153	SG	CYS	350	25.370	30.336	20.331	1.00	30.05
ATOM	1154	C	CYS	350	23.530	30.112	23.979	1.00	27.44
ATOM	1155	O	CYS	350	24.280	29.596	24.806	1.00	25.65
ATOM	1156	N	SER	351	22.551	30.944	24.316	1.00	28.30
ATOM	1157	CA	SER	351	22.341	31.321	25.716	1.00	29.76
ATOM	1158	CB	SER	351	21.239	32.377	25.835	1.00	27.97
ATOM	1159	OG	SER	351	19.972	31.819	25.545	1.00	27.29
ATOM	1160	C	SER	351	21.998	30.143	26.618	1.00	30.56
ATOM	1161	O	SER	351	22.104	30.253	27.835	1.00	30.76
ATOM	1162	N	LEU	352	21.582	29.027	26.030	1.00	30.81
ATOM	1163	CA	LEU	352	21.232	27.848	26.815	1.00	30.42
ATOM	1164	CB	LEU	352	20.275	26.948	26.035	1.00	31.12
ATOM	1165	CG	LEU	352	19.035	27.615	25.410	1.00	31.69
ATOM	1166	CD1	LEU	352	18.055	26.553	24.966	1.00	31.69
ATOM	1167	CD2	LEU	352	18.377	28.538	26.411	1.00	33.44
ATOM	1168	C	LEU	352	22.479	27.071	27.206	1.00	30.67
ATOM	1169	O	LEU	352	22.429	26.195	28.070	1.00	31.08
ATOM	1170	N	GLN	353	23.600	27.389	26.565	1.00	30.60
ATOM	1171	CA	GLN	353	24.871	26.733	26.869	1.00	31.59
ATOM	1172	CB	GLN	353	25.265	27.050	28.315	1.00	34.06
ATOM	1173	CG	GLN	353	25.542	28.519	28.575	1.00	37.01
ATOM	1174	CD	GLN	353	26.850	28.959	27.955	1.00	39.88
ATOM	1175	OE1	GLN	353	27.890	28.318	28.156	1.00	43.06
ATOM	1176	NE2	GLN	353	26.818	30.061	27.209	1.00	41.20
ATOM	1177	C	GLN	353	24.865	25.220	26.661	1.00	30.89
ATOM	1178	O	GLN	353	25.382	24.469	27.486	1.00	30.05
ATOM	1179	N	LEU	354	24.294	24.772	25.550	1.00	28.93
ATOM	1180	CA	LEU	354	24.229	23.349	25.268	1.00	27.99
ATOM	1181	CB	LEU	354	23.373	23.082	24.026	1.00	28.43
ATOM	1182	CG	LEU	354	21.881	23.406	24.046	1.00	30.02
ATOM	1183	CD1	LEU	354	21.316	23.088	22.659	1.00	30.63
ATOM	1184	CD2	LEU	354	21.156	22.608	25.114	1.00	29.61
ATOM	1185	C	LEU	354	25.604	22.736	25.039	1.00	27.41
ATOM	1186	O	LEU	354	26.540	23.415	24.604	1.00	27.14
ATOM	1187	N	THR	355	25.711	21.452	25.359	1.00	25.55
ATOM	1188	CA	THR	355	26.933	20.693	25.147	1.00	24.53
ATOM	1189	CB	THR	355	27.121	19.573	26.199	1.00	24.00
ATOM	1190	OG1	THR	355	26.116	18.564	26.015	1.00	23.40
ATOM	1191	CG2	THR	355	27.017	20.136	27.603	1.00	24.13
ATOM	1192	C	THR	355	26.750	20.026	23.785	1.00	24.40
ATOM	1193	O	THR	355	25.650	20.047	23.226	1.00	23.30
ATOM	1194	N	GLU	356	27.816	19.427	23.263	1.00	22.46
ATOM	1195	CA	GLU	356	27.754	18.756	21.971	1.00	24.63
ATOM	1196	CB	GLU	356	29.141	18.242	21.582	1.00	24.58
ATOM	1197	CG	GLU	356	30.075	19.358	21.170	1.00	26.29
ATOM	1198	CD	GLU	356	29.831	19.832	19.745	1.00	23.74
ATOM	1199	OE1	GLU	356	30.390	19.223	18.820	1.00	26.81
ATOM	1200	OE2	GLU	356	29.078	20.806	19.548	1.00	25.33
ATOM	1201	C	GLU	356	26.752	17.610	21.942	1.00	24.03
ATOM	1202	O	GLU	356	26.081	17.400	20.933	1.00	23.02
ATOM	1203	N	GLU	357	26.657	16.865	23.042	1.00	25.24
ATOM	1204	CA	GLU	357	25.721	15.746	23.122	1.00	25.24
ATOM	1205	CB	GLU	357	25.870	15.011	24.460	1.00	25.58
ATOM	1206	CG	GLU	357	27.261	14.435	24.698	1.00	28.22
ATOM	1207	CD	GLU	357	27.358	13.628	25.991	1.00	29.57
ATOM	1208	OE1	GLU	357	26.600	13.913	26.936	1.00	28.40
ATOM	1209	OE2	GLU	357	28.210	12.712	26.064	1.00	31.71
ATOM	1210	C	GLU	357	24.288	16.244	22.979	1.00	24.57
ATOM	1211	O	GLU	357	23.472	15.633	22.296	1.00	24.04
ATOM	1212	N	GLU	358	23.989	17.359	23.628	1.00	25.23
ATOM	1213	CA	GLU	358	22.655	17.933	23.560	1.00	25.61
ATOM	1214	CB	GLU	358	22.508	18.998	24.639	1.00	27.12
ATOM	1215	CG	GLU	358	22.943	18.437	25.982	1.00	29.78
ATOM	1216	CD	GLU	358	22.986	19.447	27.078	1.00	31.57
ATOM	1217	OE1	GLU	358	23.395	20.605	26.822	1.00	32.27
ATOM	1218	OE2	GLU	358	22.632	19.067	28.215	1.00	32.12
ATOM	1219	C	GLU	358	22.371	18.491	22.169	1.00	24.96
ATOM	1220	O	GLU	358	21.254	18.349	21.668	1.00	24.25
ATOM	1221	N	ILE	359	23.371	19.113	21.542	1.00	22.67
ATOM	1222	CA	ILE	359	23.188	19.645	20.191	1.00	22.78
ATOM	1223	CB	ILE	359	24.404	20.490	19.744	1.00	23.34
ATOM	1224	CG2	ILE	359	24.344	20.740	18.236	1.00	22.93
ATOM	1225	CG1	ILE	359	24.430	21.803	20.538	1.00	25.31
ATOM	1226	CD1	ILE	359	25.711	22.603	20.401	1.00	27.90
ATOM	1227	C	ILE	359	23.000	18.481	19.215	1.00	21.51
ATOM	1228	O	ILE	359	22.223	18.570	18.272	1.00	21.39
ATOM	1229	N	ALA	360	23.725	17.393	19.455	1.00	20.70
ATOM	1230	CA	ALA	360	23.629	16.208	18.617	1.00	20.02
ATOM	1231	CB	ALA	360	24.617	15.140	19.104	1.00	19.77
ATOM	1232	C	ALA	360	22.198	15.675	18.688	1.00	19.38

ATOM	1233	O	ALA	360	21.528	15.540	17.665	1.00	18.92
ATOM	1234	N	LEU	361	21.736	15.393	19.903	1.00	18.99
ATOM	1235	CA	LEU	361	20.388	14.870	20.117	1.00	19.89
ATOM	1236	CB	LEU	361	20.184	14.533	21.600	1.00	20.98
ATOM	1237	CG	LEU	361	21.138	13.452	22.105	1.00	22.49
ATOM	1238	CD1	LEU	361	20.951	13.265	23.592	1.00	23.19
ATOM	1239	CD2	LEU	361	20.882	12.151	21.358	1.00	22.76
ATOM	1240	C	LEU	361	19.285	15.817	19.642	1.00	19.52
ATOM	1241	O	LEU	361	18.374	15.402	18.933	1.00	18.57
ATOM	1242	N	PHE	362	19.356	17.085	20.030	1.00	19.75
ATOM	1243	CA	PHE	362	18.335	18.030	19.595	1.00	20.87
ATOM	1244	CB	PHE	362	18.559	19.409	20.212	1.00	19.97
ATOM	1245	CG	PHE	362	17.537	20.429	19.788	1.00	20.58
ATOM	1246	CD1	PHE	362	16.186	20.224	20.036	1.00	22.23
ATOM	1247	CD2	PHE	362	17.925	21.590	19.127	1.00	21.76
ATOM	1248	CE1	PHE	362	15.240	21.156	19.634	1.00	21.84
ATOM	1249	CE2	PHE	362	16.984	22.528	18.724	1.00	23.51
ATOM	1250	CZ	PHE	362	15.640	22.314	18.974	1.00	21.56
ATOM	1251	C	PHE	362	18.306	18.161	18.067	1.00	20.26
ATOM	1252	O	PHE	362	17.233	18.189	17.461	1.00	21.41
ATOM	1253	N	SER	363	19.476	18.253	17.445	1.00	19.81
ATOM	1254	CA	SER	363	19.521	18.371	15.991	1.00	20.02
ATOM	1255	CB	SER	363	20.963	18.572	15.498	1.00	18.56
ATOM	1256	OG	SER	363	21.728	17.396	15.663	1.00	20.81
ATOM	1257	C	SER	363	18.906	17.121	15.353	1.00	20.59
ATOM	1258	O	SER	363	18.231	17.217	14.325	1.00	20.37
ATOM	1259	N	SER	364	19.124	15.954	15.957	1.00	19.20
ATOM	1260	CA	SER	364	18.541	14.729	15.406	1.00	20.84
ATOM	1261	CB	SER	364	19.108	13.474	16.099	1.00	20.81
ATOM	1262	OG	SER	364	18.644	13.335	17.426	1.00	21.39
ATOM	1263	C	SER	364	17.007	14.772	15.538	1.00	20.41
ATOM	1264	O	SER	364	16.293	14.283	14.662	1.00	20.80
ATOM	1265	N	ALA	365	16.503	15.374	16.614	1.00	20.02
ATOM	1266	CA	ALA	365	15.053	15.484	16.813	1.00	20.02
ATOM	1267	CB	ALA	365	14.734	15.950	18.227	1.00	20.30
ATOM	1268	C	ALA	365	14.450	16.455	15.794	1.00	21.11
ATOM	1269	O	ALA	365	13.337	16.252	15.324	1.00	19.92
ATOM	1270	N	VAL	366	15.189	17.509	15.458	1.00	20.57
ATOM	1271	CA	VAL	366	14.720	18.473	14.468	1.00	19.45
ATOM	1272	CB	VAL	366	15.684	19.677	14.360	1.00	19.15
ATOM	1273	CG1	VAL	366	15.369	20.502	13.106	1.00	19.19
ATOM	1274	CG2	VAL	366	15.567	20.542	15.618	1.00	20.02
ATOM	1275	C	VAL	366	14.617	17.786	13.107	1.00	19.50
ATOM	1276	O	VAL	366	13.686	18.038	12.352	1.00	19.45
ATOM	1277	N	LEU	367	15.576	16.911	12.811	1.00	19.31
ATOM	1278	CA	LEU	367	15.602	16.176	11.550	1.00	21.04
ATOM	1279	CB	LEU	367	16.975	15.534	11.335	1.00	21.11
ATOM	1280	CG	LEU	367	17.117	14.679	10.070	1.00	21.76
ATOM	1281	CD1	LEU	367	17.139	15.585	8.841	1.00	24.04
ATOM	1282	CD2	LEU	367	18.395	13.868	10.138	1.00	19.99
ATOM	1283	C	LEU	367	14.540	15.073	11.520	1.00	20.91
ATOM	1284	O	LEU	367	13.819	14.924	10.541	1.00	19.56
ATOM	1285	N	ILE	368	14.472	14.297	12.596	1.00	20.91
ATOM	1286	CA	ILE	368	13.521	13.199	12.699	1.00	21.53
ATOM	1287	CB	ILE	368	14.047	12.095	13.649	1.00	22.94
ATOM	1288	CG2	ILE	368	13.171	10.867	13.550	1.00	22.23
ATOM	1289	CG1	ILE	368	15.499	11.735	13.308	1.00	24.46
ATOM	1290	CD1	ILE	368	15.719	11.309	11.896	1.00	27.21
ATOM	1291	C	ILE	368	12.183	13.722	13.231	1.00	22.51
ATOM	1292	O	ILE	368	11.830	13.501	14.393	1.00	21.63
ATOM	1293	N	SER	369	11.446	14.424	12.370	1.00	22.24
ATOM	1294	CA	SER	369	10.155	14.986	12.750	1.00	24.12
ATOM	1295	CB	SER	369	10.063	16.449	12.332	1.00	24.27
ATOM	1296	OG	SER	369	8.745	16.929	12.528	1.00	26.59
ATOM	1297	C	SER	369	9.011	14.221	12.107	1.00	25.22
ATOM	1298	O	SER	369	8.921	14.140	10.884	1.00	23.14
ATOM	1299	N	PRO	370	8.117	13.646	12.929	1.00	27.45
ATOM	1300	CD	PRO	370	8.169	13.553	14.402	1.00	28.35
ATOM	1301	CA	PRO	370	6.981	12.888	12.393	1.00	28.35
ATOM	1302	CB	PRO	370	6.488	12.105	13.607	1.00	28.25
ATOM	1303	CG	PRO	370	6.765	13.054	14.746	1.00	29.61
ATOM	1304	C	PRO	370	5.906	13.791	11.812	1.00	29.35
ATOM	1305	O	PRO	370	4.920	13.310	11.254	1.00	29.26
ATOM	1306	N	ASP	371	6.107	15.096	11.944	1.00	29.51
ATOM	1307	CA	ASP	371	5.151	16.074	11.450	1.00	30.84
ATOM	1308	CB	ASP	371	5.132	17.296	12.377	1.00	32.99
ATOM	1309	CG	ASP	371	4.616	16.962	13.765	1.00	35.86
ATOM	1310	OD1	ASP	371	3.508	16.390	13.853	1.00	36.71
ATOM	1311	OD2	ASP	371	5.311	17.270	14.763	1.00	37.76
ATOM	1312	C	ASP	371	5.355	16.549	10.007	1.00	29.75
ATOM	1313	O	ASP	371	4.515	17.276	9.484	1.00	30.14
ATOM	1314	N	ARG	372	6.455	16.162	9.364	1.00	28.07
ATOM	1315	CA	ARG	372	6.694	16.597	7.988	1.00	26.59
ATOM	1316	CB	ARG	372	8.030	16.075	7.458	1.00	25.22
ATOM	1317	CG	ARG	372	9.252	16.430	8.291	1.00	23.03
ATOM	1318	CD	ARG	372	9.412	17.926	8.486	1.00	22.25

ATOM	1319	NE	ARG	372	10.732	18.209	9.049	1.00	21.70
ATOM	1320	CZ	ARG	372	11.160	19.412	9.412	1.00	21.40
ATOM	1321	NH1	ARG	372	10.374	20.472	9.278	1.00	19.74
ATOM	1322	NH2	ARG	372	12.378	19.547	9.915	1.00	19.59
ATOM	1323	C	ARG	372	5.590	16.079	7.081	1.00	27.64
ATOM	1324	O	ARG	372	5.186	14.917	7.172	1.00	26.49
ATOM	1325	N	ALA	373	5.120	16.943	6.193	1.00	27.44
ATOM	1326	CA	ALA	373	4.074	16.563	5.259	1.00	27.38
ATOM	1327	CB	ALA	373	3.603	17.789	4.508	1.00	28.35
ATOM	1328	C	ALA	373	4.585	15.504	4.276	1.00	26.33
ATOM	1329	O	ALA	373	5.770	15.464	3.945	1.00	26.14
ATOM	1330	N	TRP	374	3.681	14.637	3.830	1.00	26.51
ATOM	1331	CA	TRP	374	3.987	13.582	2.856	1.00	25.94
ATOM	1332	CB	TRP	374	4.795	14.153	1.674	1.00	28.23
ATOM	1333	CG	TRP	374	4.231	15.435	1.047	1.00	30.91
ATOM	1334	CD2	TRP	374	3.112	15.543	0.146	1.00	31.01
ATOM	1335	CE2	TRP	374	2.936	16.922	-0.144	1.00	31.51
ATOM	1336	CE3	TRP	374	2.240	14.614	-0.438	1.00	30.75
ATOM	1337	CD1	TRP	374	4.676	16.718	1.252	1.00	31.80
ATOM	1338	NE1	TRP	374	3.903	17.614	0.541	1.00	31.78
ATOM	1339	CZ2	TRP	374	1.920	17.390	-0.998	1.00	31.60
ATOM	1340	CZ3	TRP	374	1.223	15.082	-1.289	1.00	32.14
ATOM	1341	CH2	TRP	374	1.075	16.458	-1.556	1.00	31.37
ATOM	1342	C	TRP	374	4.690	12.310	3.365	1.00	24.31
ATOM	1343	O	TRP	374	4.926	11.384	2.588	1.00	23.56
ATOM	1344	N	LEU	375	5.039	12.258	4.648	1.00	24.62
ATOM	1345	CA	LEU	375	5.698	11.070	5.185	1.00	24.04
ATOM	1346	CB	LEU	375	6.074	11.282	6.657	1.00	24.87
ATOM	1347	CG	LEU	375	7.256	12.194	7.022	1.00	24.99
ATOM	1348	CD1	LEU	375	7.422	12.210	8.542	1.00	25.00
ATOM	1349	CD2	LEU	375	8.543	11.686	6.367	1.00	25.29
ATOM	1350	C	LEU	375	4.769	9.853	5.065	1.00	23.50
ATOM	1351	O	LEU	375	3.584	9.946	5.366	1.00	23.84
ATOM	1352	N	LEU	376	5.318	8.721	4.632	1.00	23.94
ATOM	1353	CA	LEU	376	4.540	7.489	4.471	1.00	24.75
ATOM	1354	CB	LEU	376	5.202	6.595	3.423	1.00	24.43
ATOM	1355	CG	LEU	376	5.268	7.172	2.001	1.00	26.18
ATOM	1356	CD1	LEU	376	6.160	6.296	1.124	1.00	27.91
ATOM	1357	CD2	LEU	376	3.858	7.260	1.415	1.00	26.56
ATOM	1358	C	LEU	376	4.355	6.711	5.783	1.00	25.66
ATOM	1359	O	LEU	376	3.317	6.079	6.002	1.00	24.55
ATOM	1360	N	GLU	377	5.359	6.758	6.654	1.00	26.36
ATOM	1361	CA	GLU	377	5.284	6.063	7.938	1.00	27.47
ATOM	1362	CB	GLU	377	6.261	4.878	7.947	1.00	29.08
ATOM	1363	CG	GLU	377	5.959	3.840	6.875	1.00	30.40
ATOM	1364	CD	GLU	377	6.773	2.574	7.010	1.00	32.62
ATOM	1365	OE1	GLU	377	7.981	2.578	6.704	1.00	33.66
ATOM	1366	OE2	GLU	377	6.197	1.556	7.428	1.00	33.92
ATOM	1367	C	GLU	377	5.602	7.037	9.077	1.00	27.62
ATOM	1368	O	GLU	377	6.619	6.902	9.762	1.00	27.21
ATOM	1369	N	PRO	378	4.728	8.035	9.295	1.00	27.83
ATOM	1370	CD	PRO	378	3.483	8.329	8.561	1.00	27.90
ATOM	1371	CA	PRO	378	4.951	9.020	10.358	1.00	28.17
ATOM	1372	CB	PRO	378	3.794	10.004	10.167	1.00	29.14
ATOM	1373	CG	PRO	378	2.707	9.143	9.564	1.00	28.27
ATOM	1374	C	PRO	378	5.015	8.458	11.776	1.00	29.36
ATOM	1375	O	PRO	378	5.655	9.050	12.649	1.00	28.11
ATOM	1376	N	ARG	379	4.349	7.328	12.008	1.00	28.75
ATOM	1377	CA	ARG	379	4.339	6.714	13.331	1.00	30.40
ATOM	1378	CB	ARG	379	3.327	5.551	13.366	1.00	32.82
ATOM	1379	CG	ARG	379	2.361	5.554	14.559	1.00	38.05
ATOM	1380	CD	ARG	379	3.009	5.102	15.888	1.00	42.49
ATOM	1381	NE	ARG	379	3.379	6.216	16.779	1.00	45.57
ATOM	1382	CZ	ARG	379	3.867	6.071	18.014	1.00	47.28
ATOM	1383	NH1	ARG	379	4.062	4.858	18.530	1.00	48.40
ATOM	1384	NH2	ARG	379	4.145	7.142	18.752	1.00	48.86
ATOM	1385	C	ARG	379	5.741	6.199	13.652	1.00	29.02
ATOM	1386	O	ARG	379	6.230	6.334	14.773	1.00	29.03
ATOM	1387	N	LYS	380	6.377	5.611	12.647	1.00	28.46
ATOM	1388	CA	LYS	380	7.706	5.058	12.791	1.00	29.03
ATOM	1389	CB	LYS	380	8.109	4.391	11.481	1.00	30.34
ATOM	1390	CG	LYS	380	9.086	3.254	11.621	1.00	33.47
ATOM	1391	CD	LYS	380	9.080	2.353	10.379	1.00	34.27
ATOM	1392	CE	LYS	380	7.739	1.647	10.196	1.00	35.69
ATOM	1393	NZ	LYS	380	7.814	0.565	9.162	1.00	37.30
ATOM	1394	C	LYS	380	8.657	6.196	13.137	1.00	29.26
ATOM	1395	O	LYS	380	9.528	6.049	13.999	1.00	30.09
ATOM	1396	N	VAL	381	8.480	7.330	12.466	1.00	27.49
ATOM	1397	CA	VAL	381	9.314	8.501	12.713	1.00	27.12
ATOM	1398	CB	VAL	381	9.054	9.617	11.663	1.00	26.02
ATOM	1399	CG1	VAL	381	9.821	10.888	12.038	1.00	25.31
ATOM	1400	CG2	VAL	381	9.494	9.140	10.280	1.00	25.42
ATOM	1401	C	VAL	381	9.014	9.047	14.104	1.00	27.48
ATOM	1402	O	VAL	381	9.914	9.478	14.830	1.00	26.45
ATOM	1403	N	GLN	382	7.743	9.014	14.475	1.00	28.11
ATOM	1404	CA	GLN	382	7.324	9.508	15.775	1.00	29.95

ATOM	1405	CB	GLN	382	5.803	9.505	15.873	1.00	31.75
ATOM	1406	CG	GLN	382	5.302	10.011	17.202	1.00	35.79
ATOM	1407	CD	GLN	382	3.886	10.501	17.117	1.00	38.98
ATOM	1408	OE1	GLN	382	2.978	9.761	16.711	1.00	40.59
ATOM	1409	NE2	GLN	382	3.677	11.765	17.487	1.00	40.58
ATOM	1410	C	GLN	382	7.907	8.707	16.931	1.00	29.66
ATOM	1411	O	GLN	382	8.323	9.278	17.943	1.00	28.76
ATOM	1412	N	LYS	383	7.922	7.385	16.776	1.00	29.16
ATOM	1413	CA	LYS	383	8.454	6.491	17.799	1.00	29.20
ATOM	1414	CB	LYS	383	8.303	5.027	17.369	1.00	30.44
ATOM	1415	CG	LYS	383	6.860	4.503	17.326	1.00	33.92
ATOM	1416	CD	LYS	383	6.810	3.149	16.627	1.00	37.33
ATOM	1417	CE	LYS	383	5.486	2.419	16.837	1.00	39.20
ATOM	1418	NZ	LYS	383	5.439	1.665	18.135	1.00	40.75
ATOM	1419	C	LYS	383	9.928	6.785	18.055	1.00	28.39
ATOM	1420	O	LYS	383	10.370	6.781	19.202	1.00	28.89
ATOM	1421	N	LEU	384	10.692	7.019	16.990	1.00	26.11
ATOM	1422	CA	LEU	384	12.117	7.324	17.138	1.00	25.71
ATOM	1423	CB	LEU	384	12.829	7.235	15.778	1.00	23.95
ATOM	1424	CG	LEU	384	14.332	7.536	15.718	1.00	22.17
ATOM	1425	CD1	LEU	384	15.102	6.661	16.719	1.00	24.02
ATOM	1426	CD2	LEU	384	14.833	7.285	14.299	1.00	21.00
ATOM	1427	C	LEU	384	12.330	8.711	17.760	1.00	25.43
ATOM	1428	O	LEU	384	13.157	8.867	18.663	1.00	25.70
ATOM	1429	N	GLN	385	11.591	9.714	17.294	1.00	24.38
ATOM	1430	CA	GLN	385	11.748	11.054	17.846	1.00	24.43
ATOM	1431	CB	GLN	385	10.819	12.072	17.167	1.00	24.78
ATOM	1432	CG	GLN	385	11.260	13.503	17.459	1.00	22.10
ATOM	1433	CD	GLN	385	10.221	14.561	17.136	1.00	23.15
ATOM	1434	OE1	GLN	385	10.528	15.569	16.498	1.00	24.07
ATOM	1435	NE2	GLN	385	8.996	14.350	17.592	1.00	19.99
ATOM	1436	C	GLN	385	11.449	11.040	19.347	1.00	24.85
ATOM	1437	O	GLN	385	12.101	11.731	20.125	1.00	23.88
ATOM	1438	N	GLU	386	10.449	10.265	19.745	1.00	25.17
ATOM	1439	CA	GLU	386	10.093	10.170	21.159	1.00	27.06
ATOM	1440	CB	GLU	386	8.902	9.237	21.355	1.00	30.30
ATOM	1441	CG	GLU	386	7.581	9.951	21.578	1.00	36.42
ATOM	1442	CD	GLU	386	6.470	8.966	21.878	1.00	40.38
ATOM	1443	OE1	GLU	386	5.997	8.309	20.923	1.00	42.90
ATOM	1444	OE2	GLU	386	6.094	8.828	23.068	1.00	43.27
ATOM	1445	C	GLU	386	11.271	9.661	21.978	1.00	25.28
ATOM	1446	O	GLU	386	11.563	10.198	23.044	1.00	25.32
ATOM	1447	N	LYS	387	11.932	8.619	21.476	1.00	23.39
ATOM	1448	CA	LYS	387	13.088	8.038	22.148	1.00	24.19
ATOM	1449	CB	LYS	387	13.532	6.769	21.434	1.00	24.48
ATOM	1450	CG	LYS	387	12.526	5.645	21.544	1.00	25.85
ATOM	1451	CD	LYS	387	12.849	4.512	20.605	1.00	26.31
ATOM	1452	CE	LYS	387	11.751	3.477	20.656	1.00	25.95
ATOM	1453	NZ	LYS	387	11.950	2.448	19.620	1.00	27.79
ATOM	1454	C	LYS	387	14.244	9.031	22.191	1.00	24.21
ATOM	1455	O	LYS	387	14.972	9.104	23.175	1.00	21.82
ATOM	1456	N	ILE	388	14.410	9.783	21.109	1.00	23.57
ATOM	1457	CA	ILE	388	15.465	10.786	21.033	1.00	23.44
ATOM	1458	CB	ILE	388	15.484	11.463	19.637	1.00	21.69
ATOM	1459	CG2	ILE	388	16.394	12.678	19.646	1.00	22.46
ATOM	1460	CG1	ILE	388	15.936	10.449	18.588	1.00	23.21
ATOM	1461	CD1	ILE	388	15.987	11.002	17.186	1.00	23.27
ATOM	1462	C	ILE	388	15.234	11.840	22.113	1.00	22.84
ATOM	1463	O	ILE	388	16.145	12.173	22.872	1.00	22.21
ATOM	1464	N	TYR	389	14.009	12.351	22.198	1.00	22.43
ATOM	1465	CA	TYR	389	13.695	13.363	23.197	1.00	24.16
ATOM	1466	CB	TYR	389	12.268	13.868	23.003	1.00	25.05
ATOM	1467	CG	TYR	389	12.164	14.996	22.000	1.00	26.11
ATOM	1468	CD1	TYR	389	11.102	15.057	21.093	1.00	26.57
ATOM	1469	CE1	TYR	389	10.971	16.124	20.203	1.00	25.71
ATOM	1470	CD2	TYR	389	13.101	16.037	21.990	1.00	28.12
ATOM	1471	CE2	TYR	389	12.975	17.115	21.102	1.00	27.45
ATOM	1472	CZ	TYR	389	11.906	17.149	20.215	1.00	26.96
ATOM	1473	OH	TYR	389	11.754	18.218	19.356	1.00	28.94
ATOM	1474	C	TYR	389	13.876	12.802	24.607	1.00	24.83
ATOM	1475	O	TYR	389	14.337	13.502	25.503	1.00	24.78
ATOM	1476	N	PHE	390	13.514	11.537	24.794	1.00	25.27
ATOM	1477	CA	PHE	390	13.672	10.908	26.100	1.00	27.07
ATOM	1478	CB	PHE	390	13.150	9.469	26.070	1.00	29.52
ATOM	1479	CG	PHE	390	11.710	9.331	26.499	1.00	33.25
ATOM	1480	CD1	PHE	390	10.839	8.482	25.807	1.00	34.80
ATOM	1481	CD2	PHE	390	11.230	10.029	27.609	1.00	34.21
ATOM	1482	CE1	PHE	390	9.499	8.325	26.208	1.00	35.97
ATOM	1483	CE2	PHE	390	9.895	9.882	28.025	1.00	37.03
ATOM	1484	CZ	PHE	390	9.027	9.025	27.319	1.00	35.82
ATOM	1485	C	PHE	390	15.156	10.929	26.451	1.00	25.45
ATOM	1486	O	PHE	390	15.531	11.227	27.584	1.00	23.68
ATOM	1487	N	ALA	391	15.991	10.625	25.461	1.00	24.65
ATOM	1488	CA	ALA	391	17.432	10.627	25.658	1.00	24.20
ATOM	1489	CB	ALA	391	18.141	10.116	24.414	1.00	24.05
ATOM	1490	C	ALA	391	17.907	12.036	25.989	1.00	24.18

ATOM	1491	O	ALA	391	18.650	12.232	26.951	1.00	25.43
ATOM	1492	N	LEU	392	17.465	13.014	25.201	1.00	24.17
ATOM	1493	CA	LEU	392	17.857	14.402	25.410	1.00	23.73
ATOM	1494	CB	LEU	392	17.178	15.309	24.375	1.00	23.42
ATOM	1495	CG	LEU	392	17.432	16.815	24.510	1.00	21.24
ATOM	1496	CD1	LEU	392	18.928	17.097	24.423	1.00	21.69
ATOM	1497	CD2	LEU	392	16.672	17.571	23.423	1.00	22.29
ATOM	1498	C	LEU	392	17.506	14.868	26.819	1.00	25.25
ATOM	1499	O	LEU	392	18.293	15.549	27.474	1.00	24.27
ATOM	1500	N	GLN	393	16.323	14.485	27.288	1.00	25.02
ATOM	1501	CA	GLN	393	15.864	14.873	28.614	1.00	26.69
ATOM	1502	CB	GLN	393	14.439	14.366	28.818	1.00	29.39
ATOM	1503	CG	GLN	393	13.773	14.865	30.074	1.00	34.04
ATOM	1504	CD	GLN	393	12.294	14.569	30.079	1.00	36.82
ATOM	1505	OE1	GLN	393	11.880	13.411	29.996	1.00	37.30
ATOM	1506	NE2	GLN	393	11.484	15.617	30.167	1.00	38.82
ATOM	1507	C	GLN	393	16.783	14.349	29.724	1.00	26.46
ATOM	1508	O	GLN	393	17.019	15.040	30.710	1.00	25.57
ATOM	1509	N	HIS	394	17.287	13.128	29.572	1.00	25.89
ATOM	1510	CA	HIS	394	18.190	12.559	30.569	1.00	26.72
ATOM	1511	CB	HIS	394	18.314	11.049	30.375	1.00	27.82
ATOM	1512	CG	HIS	394	17.087	10.289	30.776	1.00	31.60
ATOM	1513	CD2	HIS	394	15.994	9.927	30.065	1.00	31.53
ATOM	1514	ND1	HIS	394	16.873	9.841	32.063	1.00	33.22
ATOM	1515	CE1	HIS	394	15.702	9.238	32.127	1.00	33.60
ATOM	1516	NE2	HIS	394	15.146	9.276	30.929	1.00	34.06
ATOM	1517	C	HIS	394	19.567	13.208	30.491	1.00	25.56
ATOM	1518	O	HIS	394	20.155	13.552	31.513	1.00	25.72
ATOM	1519	N	VAL	395	20.082	13.385	29.274	1.00	25.55
ATOM	1520	CA	VAL	395	21.402	13.993	29.094	1.00	24.89
ATOM	1521	CB	VAL	395	21.821	13.992	27.599	1.00	25.87
ATOM	1522	CG1	VAL	395	23.094	14.815	27.399	1.00	25.30
ATOM	1523	CG2	VAL	395	22.056	12.554	27.134	1.00	25.17
ATOM	1524	C	VAL	395	21.461	15.426	29.633	1.00	25.38
ATOM	1525	O	VAL	395	22.476	15.847	30.185	1.00	23.83
ATOM	1526	N	ILE	396	20.366	16.162	29.488	1.00	24.76
ATOM	1527	CA	ILE	396	20.310	17.542	29.956	1.00	25.56
ATOM	1528	CB	ILE	396	18.953	18.180	29.588	1.00	25.31
ATOM	1529	CG2	ILE	396	18.725	19.465	30.382	1.00	24.55
ATOM	1530	CG1	ILE	396	18.910	18.465	28.080	1.00	24.97
ATOM	1531	CD1	ILE	396	17.556	18.989	27.593	1.00	24.29
ATOM	1532	C	ILE	396	20.531	17.635	31.471	1.00	28.65
ATOM	1533	O	ILE	396	21.134	18.583	31.960	1.00	28.05
ATOM	1534	N	GLN	397	20.046	16.639	32.203	1.00	31.32
ATOM	1535	CA	GLN	397	20.191	16.609	33.656	1.00	35.38
ATOM	1536	CB	GLN	397	19.472	15.393	34.221	1.00	36.34
ATOM	1537	CG	GLN	397	18.056	15.243	33.752	1.00	39.24
ATOM	1538	CD	GLN	397	17.387	14.038	34.382	1.00	42.16
ATOM	1539	OE1	GLN	397	17.995	12.971	34.522	1.00	42.62
ATOM	1540	NE2	GLN	397	16.125	14.195	34.755	1.00	43.91
ATOM	1541	C	GLN	397	21.640	16.577	34.143	1.00	37.04
ATOM	1542	O	GLN	397	21.936	17.049	35.240	1.00	37.11
ATOM	1543	N	LYS	398	22.533	15.993	33.350	1.00	39.23
ATOM	1544	CA	LYS	398	23.945	15.915	33.733	1.00	42.23
ATOM	1545	CB	LYS	398	24.742	15.089	32.720	1.00	40.46
ATOM	1546	CG	LYS	398	24.193	13.689	32.476	1.00	39.92
ATOM	1547	CD	LYS	398	25.170	12.833	31.675	1.00	39.62
ATOM	1548	CE	LYS	398	25.430	13.434	30.286	1.00	39.22
ATOM	1549	NZ	LYS	398	26.362	12.596	29.484	1.00	37.98
ATOM	1550	C	LYS	398	24.557	17.306	33.818	1.00	44.28
ATOM	1551	O	LYS	398	25.543	17.535	34.529	1.00	44.44
ATOM	1552	N	ASN	399	23.964	18.241	33.091	1.00	45.83
ATOM	1553	CA	ASN	399	24.469	19.595	33.063	1.00	47.39
ATOM	1554	CB	ASN	399	24.734	19.967	31.604	1.00	47.57
ATOM	1555	CG	ASN	399	25.348	18.807	30.803	1.00	47.79
ATOM	1556	OD1	ASN	399	26.505	18.434	31.010	1.00	47.93
ATOM	1557	ND2	ASN	399	24.564	18.226	29.896	1.00	48.24
ATOM	1558	C	ASN	399	23.474	20.560	33.710	1.00	49.01
ATOM	1559	O	ASN	399	23.431	20.717	34.937	1.00	49.34
ATOM	1560	N	HIS	400	22.671	21.186	32.861	1.00	50.43
ATOM	1561	CA	HIS	400	21.655	22.160	33.240	1.00	52.29
ATOM	1562	CB	HIS	400	20.737	22.349	32.046	1.00	51.08
ATOM	1563	CG	HIS	400	21.475	22.344	30.750	1.00	50.35
ATOM	1564	CD2	HIS	400	21.653	21.368	29.832	1.00	50.24
ATOM	1565	ND1	HIS	400	22.219	23.419	30.316	1.00	50.79
ATOM	1566	CE1	HIS	400	22.823	23.102	29.183	1.00	50.91
ATOM	1567	NE2	HIS	400	22.495	21.862	28.871	1.00	49.91
ATOM	1568	C	HIS	400	20.839	21.782	34.467	1.00	54.62
ATOM	1569	O	HIS	400	19.881	21.006	34.369	1.00	54.65
ATOM	1570	N	LEU	401	21.211	22.343	35.618	1.00	56.91
ATOM	1571	CA	LEU	401	20.487	22.061	36.854	1.00	59.10
ATOM	1572	CB	LEU	401	21.306	22.469	38.081	1.00	59.50
ATOM	1573	CG	LEU	401	21.083	21.490	39.244	1.00	60.29
ATOM	1574	CD1	LEU	401	19.671	21.626	39.794	1.00	60.01
ATOM	1575	CD2	LEU	401	21.317	20.062	38.748	1.00	59.79
ATOM	1576	C	LEU	401	19.224	22.890	36.729	1.00	60.18

ATOM	1577	O	LEU	401	19.275	24.017	36.220	1.00	61.06
ATOM	1578	N	ASP	402	18.097	22.341	37.188	1.00	60.81
ATOM	1579	CA	ASP	402	16.814	23.001	37.016	1.00	61.03
ATOM	1580	CB	ASP	402	16.766	24.371	37.711	1.00	62.09
ATOM	1581	CG	ASP	402	16.409	24.256	39.205	1.00	63.42
ATOM	1582	OD1	ASP	402	16.940	23.342	39.883	1.00	63.79
ATOM	1583	OD2	ASP	402	15.609	25.076	39.716	1.00	63.96
ATOM	1584	C	ASP	402	16.836	23.099	35.499	1.00	60.63
ATOM	1585	O	ASP	402	17.621	22.375	34.864	1.00	61.17
ATOM	1586	N	ASP	403	16.035	23.950	34.882	1.00	59.71
ATOM	1587	CA	ASP	403	16.083	23.943	33.430	1.00	57.97
ATOM	1588	CB	ASP	403	15.969	22.502	32.944	1.00	57.91
ATOM	1589	CG	ASP	403	14.749	21.799	33.538	1.00	58.27
ATOM	1590	OD1	ASP	403	13.789	21.500	32.785	1.00	57.61
ATOM	1591	OD2	ASP	403	14.747	21.570	34.774	1.00	57.74
ATOM	1592	C	ASP	403	15.025	24.719	32.703	1.00	56.47
ATOM	1593	O	ASP	403	15.042	25.947	32.631	1.00	56.67
ATOM	1594	N	GLU	404	14.097	23.936	32.157	1.00	54.01
ATOM	1595	CA	GLU	404	13.021	24.422	31.319	1.00	50.92
ATOM	1596	CB	GLU	404	12.788	25.917	31.554	1.00	52.53
ATOM	1597	CG	GLU	404	11.500	26.492	30.994	1.00	55.75
ATOM	1598	CD	GLU	404	11.230	27.889	31.537	1.00	57.67
ATOM	1599	OE1	GLU	404	10.211	28.503	31.134	1.00	58.54
ATOM	1600	OE2	GLU	404	12.041	28.371	32.375	1.00	58.20
ATOM	1601	C	GLU	404	13.714	24.171	29.977	1.00	47.15
ATOM	1602	O	GLU	404	13.121	24.300	28.907	1.00	46.59
ATOM	1603	N	THR	405	14.986	23.774	30.070	1.00	43.07
ATOM	1604	CA	THR	405	15.815	23.492	28.895	1.00	38.65
ATOM	1605	CB	THR	405	17.122	22.739	29.288	1.00	38.43
ATOM	1606	OG1	THR	405	17.950	23.598	30.083	1.00	36.75
ATOM	1607	CG2	THR	405	17.915	22.330	28.036	1.00	37.77
ATOM	1608	C	THR	405	15.101	22.712	27.791	1.00	35.86
ATOM	1609	O	THR	405	14.859	23.258	26.721	1.00	33.56
ATOM	1610	N	LEU	406	14.749	21.449	28.039	1.00	34.04
ATOM	1611	CA	LEU	406	14.083	20.668	27.000	1.00	32.51
ATOM	1612	CB	LEU	406	13.653	19.290	27.516	1.00	32.98
ATOM	1613	CG	LEU	406	13.758	18.137	26.500	1.00	31.34
ATOM	1614	CD1	LEU	406	12.660	17.122	26.773	1.00	32.45
ATOM	1615	CD2	LEU	406	13.645	18.644	25.077	1.00	32.35
ATOM	1616	C	LEU	406	12.856	21.395	26.456	1.00	31.91
ATOM	1617	O	LEU	406	12.625	21.414	25.253	1.00	30.54
ATOM	1618	N	ALA	407	12.070	21.988	27.348	1.00	32.12
ATOM	1619	CA	ALA	407	10.879	22.720	26.931	1.00	31.85
ATOM	1620	CB	ALA	407	10.078	23.150	28.146	1.00	31.21
ATOM	1621	C	ALA	407	11.246	23.942	26.084	1.00	31.46
ATOM	1622	O	ALA	407	10.584	24.221	25.093	1.00	31.62
ATOM	1623	N	LYS	408	12.296	24.667	26.473	1.00	31.28
ATOM	1624	CA	LYS	408	12.723	25.849	25.718	1.00	30.77
ATOM	1625	CB	LYS	408	13.794	26.635	26.481	1.00	33.47
ATOM	1626	CG	LYS	408	13.279	27.310	27.747	1.00	35.82
ATOM	1627	CD	LYS	408	14.332	28.218	28.353	1.00	36.77
ATOM	1628	CE	LYS	408	13.747	29.011	29.522	1.00	38.42
ATOM	1629	NZ	LYS	408	14.719	29.999	30.088	1.00	39.51
ATOM	1630	C	LYS	408	13.263	25.462	24.351	1.00	28.18
ATOM	1631	O	LYS	408	13.158	26.229	23.396	1.00	27.16
ATOM	1632	N	LEU	409	13.858	24.276	24.265	1.00	27.09
ATOM	1633	CA	LEU	409	14.387	23.793	22.994	1.00	26.20
ATOM	1634	CB	LEU	409	15.246	22.546	23.210	1.00	24.61
ATOM	1635	CG	LEU	409	16.608	22.793	23.844	1.00	25.33
ATOM	1636	CD1	LEU	409	17.347	21.465	24.018	1.00	23.27
ATOM	1637	CD2	LEU	409	17.399	23.757	22.957	1.00	25.46
ATOM	1638	C	LEU	409	13.228	23.462	22.057	1.00	26.11
ATOM	1639	O	LEU	409	13.184	23.928	20.916	1.00	25.38
ATOM	1640	N	ILE	410	12.289	22.657	22.548	1.00	25.80
ATOM	1641	CA	ILE	410	11.130	22.263	21.750	1.00	27.11
ATOM	1642	CB	ILE	410	10.212	21.309	22.556	1.00	27.55
ATOM	1643	CG2	ILE	410	8.831	21.225	21.915	1.00	29.14
ATOM	1644	CG1	ILE	410	10.862	19.925	22.640	1.00	28.88
ATOM	1645	CD1	ILE	410	10.227	18.999	23.672	1.00	29.04
ATOM	1646	C	ILE	410	10.324	23.477	21.271	1.00	26.54
ATOM	1647	O	ILE	410	9.801	23.483	20.157	1.00	27.28
ATOM	1648	N	ALA	411	10.240	24.504	22.108	1.00	26.52
ATOM	1649	CA	ALA	411	9.501	25.716	21.762	1.00	27.27
ATOM	1650	CB	ALA	411	9.388	26.618	22.982	1.00	28.31
ATOM	1651	C	ALA	411	10.187	26.473	20.618	1.00	28.07
ATOM	1652	O	ALA	411	9.600	27.379	20.026	1.00	27.10
ATOM	1653	N	LYS	412	11.426	26.095	20.310	1.00	27.07
ATOM	1654	CA	LYS	412	12.175	26.751	19.244	1.00	28.19
ATOM	1655	CB	LYS	412	13.680	26.756	19.579	1.00	28.62
ATOM	1656	CG	LYS	412	14.067	27.694	20.728	1.00	30.34
ATOM	1657	CD	LYS	412	15.559	27.615	21.042	1.00	31.67
ATOM	1658	CE	LYS	412	15.950	28.514	22.215	1.00	33.03
ATOM	1659	NZ	LYS	412	15.797	29.985	21.964	1.00	35.05
ATOM	1660	C	LYS	412	11.955	26.117	17.864	1.00	27.51
ATOM	1661	O	LYS	412	12.316	26.708	16.847	1.00	27.32
ATOM	1662	N	ILE	413	11.363	24.926	17.834	1.00	26.06

ATOM	1663	CA	ILE	413	11.105	24.202	16.588	1.00	26.80
ATOM	1664	CB	ILE	413	10.220	22.939	16.841	1.00	27.43
ATOM	1665	CG2	ILE	413	9.881	22.247	15.523	1.00	27.29
ATOM	1666	CG1	ILE	413	10.945	21.958	17.770	1.00	28.37
ATOM	1667	CD1	ILE	413	12.121	21.254	17.148	1.00	29.37
ATOM	1668	C	ILE	413	10.433	25.057	15.519	1.00	26.56
ATOM	1669	O	ILE	413	10.864	25.076	14.372	1.00	26.28
ATOM	1670	N	PRO	414	9.359	25.775	15.882	1.00	27.37
ATOM	1671	CD	PRO	414	8.700	25.857	17.198	1.00	26.88
ATOM	1672	CA	PRO	414	8.669	26.614	14.897	1.00	26.65
ATOM	1673	CB	PRO	414	7.427	27.080	15.658	1.00	27.87
ATOM	1674	CG	PRO	414	7.903	27.129	17.070	1.00	29.01
ATOM	1675	C	PRO	414	9.525	27.771	14.374	1.00	25.68
ATOM	1676	O	PRO	414	9.448	28.126	13.201	1.00	27.18
ATOM	1677	N	THR	415	10.352	28.342	15.241	1.00	25.08
ATOM	1678	CA	THR	415	11.226	29.448	14.850	1.00	25.70
ATOM	1679	CB	THR	415	11.944	30.028	16.089	1.00	27.08
ATOM	1680	OG1	THR	415	10.964	30.406	17.060	1.00	27.92
ATOM	1681	CG2	THR	415	12.768	31.250	15.727	1.00	26.93
ATOM	1682	C	THR	415	12.260	28.954	13.825	1.00	23.76
ATOM	1683	O	THR	415	12.546	29.624	12.839	1.00	23.92
ATOM	1684	N	ILE	416	12.801	27.768	14.072	1.00	22.76
ATOM	1685	CA	ILE	416	13.780	27.158	13.184	1.00	21.78
ATOM	1686	CB	ILE	416	14.175	25.760	13.711	1.00	22.29
ATOM	1687	CG2	ILE	416	14.921	24.976	12.648	1.00	21.98
ATOM	1688	CG1	ILE	416	15.012	25.918	14.979	1.00	20.99
ATOM	1689	CD1	ILE	416	15.190	24.634	15.776	1.00	22.24
ATOM	1690	C	ILE	416	13.187	27.041	11.785	1.00	20.31
ATOM	1691	O	ILE	416	13.790	27.454	10.797	1.00	19.18
ATOM	1692	N	THR	417	11.988	26.480	11.710	1.00	20.67
ATOM	1693	CA	THR	417	11.328	26.317	10.432	1.00	20.39
ATOM	1694	CB	THR	417	10.048	25.508	10.602	1.00	21.40
ATOM	1695	OG1	THR	417	10.390	24.228	11.147	1.00	20.70
ATOM	1696	CG2	THR	417	9.351	25.313	9.257	1.00	19.07
ATOM	1697	C	THR	417	11.026	27.661	9.785	1.00	20.61
ATOM	1698	O	THR	417	11.118	27.795	8.570	1.00	21.29
ATOM	1699	N	ALA	418	10.674	28.651	10.605	1.00	21.09
ATOM	1700	CA	ALA	418	10.367	29.987	10.118	1.00	20.90
ATOM	1701	CB	ALA	418	9.956	30.880	11.273	1.00	21.36
ATOM	1702	C	ALA	418	11.573	30.592	9.404	1.00	21.24
ATOM	1703	O	ALA	418	11.441	31.157	8.321	1.00	19.90
ATOM	1704	N	VAL	419	12.747	30.457	10.015	1.00	21.50
ATOM	1705	CA	VAL	419	13.975	30.995	9.440	1.00	21.76
ATOM	1706	CB	VAL	419	15.170	30.797	10.406	1.00	20.86
ATOM	1707	CG1	VAL	419	16.491	31.146	9.713	1.00	22.17
ATOM	1708	CG2	VAL	419	14.969	31.655	11.648	1.00	23.28
ATOM	1709	C	VAL	419	14.282	30.328	8.104	1.00	21.71
ATOM	1710	O	VAL	419	14.586	30.997	7.120	1.00	21.28
ATOM	1711	N	CYS	420	14.180	29.006	8.065	1.00	20.93
ATOM	1712	CA	CYS	420	14.467	28.282	6.840	1.00	22.24
ATOM	1713	CB	CYS	420	14.560	26.782	7.137	1.00	20.03
ATOM	1714	SG	CYS	420	15.994	26.393	8.177	1.00	21.62
ATOM	1715	C	CYS	420	13.462	28.573	5.724	1.00	22.17
ATOM	1716	O	CYS	420	13.815	28.560	4.545	1.00	22.39
ATOM	1717	N	ASN	421	12.213	28.843	6.090	1.00	22.88
ATOM	1718	CA	ASN	421	11.213	29.165	5.083	1.00	23.16
ATOM	1719	CB	ASN	421	9.803	29.189	5.686	1.00	24.82
ATOM	1720	CG	ASN	421	9.254	27.797	5.945	1.00	26.54
ATOM	1721	OD1	ASN	421	9.691	26.821	5.332	1.00	28.43
ATOM	1722	ND2	ASN	421	8.274	27.703	6.841	1.00	28.17
ATOM	1723	C	ASN	421	11.548	30.539	4.507	1.00	22.83
ATOM	1724	O	ASN	421	11.372	30.783	3.311	1.00	23.42
ATOM	1725	N	LEU	422	12.026	31.438	5.362	1.00	21.51
ATOM	1726	CA	LEU	422	12.394	32.773	4.912	1.00	21.12
ATOM	1727	CB	LEU	422	12.814	33.657	6.094	1.00	20.93
ATOM	1728	CG	LEU	422	13.106	35.117	5.724	1.00	22.12
ATOM	1729	CD1	LEU	422	11.914	35.708	4.998	1.00	23.58
ATOM	1730	CD2	LEU	422	13.420	35.919	6.968	1.00	21.92
ATOM	1731	C	LEU	422	13.539	32.651	3.909	1.00	20.79
ATOM	1732	O	LEU	422	13.589	33.385	2.924	1.00	20.16
ATOM	1733	N	HIS	423	14.457	31.721	4.162	1.00	20.32
ATOM	1734	CA	HIS	423	15.569	31.496	3.246	1.00	19.09
ATOM	1735	CB	HIS	423	16.480	30.377	3.774	1.00	19.51
ATOM	1736	CG	HIS	423	17.357	29.757	2.726	1.00	20.42
ATOM	1737	CD2	HIS	423	18.560	30.132	2.233	1.00	22.15
ATOM	1738	ND1	HIS	423	17.002	28.617	2.037	1.00	19.93
ATOM	1739	CE1	HIS	423	17.945	28.317	1.164	1.00	21.28
ATOM	1740	NE2	HIS	423	18.903	29.221	1.261	1.00	23.18
ATOM	1741	C	HIS	423	14.991	31.114	1.887	1.00	20.06
ATOM	1742	O	HIS	423	15.406	31.633	0.854	1.00	19.48
ATOM	1743	N	GLY	424	14.025	30.202	1.897	1.00	20.89
ATOM	1744	CA	GLY	424	13.409	29.779	0.656	1.00	21.77
ATOM	1745	C	GLY	424	12.747	30.948	-0.045	1.00	22.46
ATOM	1746	O	GLY	424	12.854	31.092	-1.260	1.00	22.28
ATOM	1747	N	GLU	425	12.055	31.781	0.723	1.00	23.68
ATOM	1748	CA	GLU	425	11.388	32.944	0.156	1.00	26.30

ATOM	1749	CB	GLU	425	10.654	33.714	1.254	1.00	29.71
ATOM	1750	CG	GLU	425	9.438	32.987	1.807	1.00	34.81
ATOM	1751	CD	GLU	425	8.840	33.708	3.000	1.00	39.53
ATOM	1752	OE1	GLU	425	8.732	34.960	2.940	1.00	40.10
ATOM	1753	OE2	GLU	425	8.471	33.026	3.992	1.00	42.79
ATOM	1754	C	GLU	425	12.380	33.862	-0.553	1.00	25.74
ATOM	1755	O	GLU	425	12.166	34.228	-1.708	1.00	26.36
ATOM	1756	N	LYS	426	13.468	34.221	0.125	1.00	25.26
ATOM	1757	CA	LYS	426	14.484	35.094	-0.470	1.00	25.80
ATOM	1758	CB	LYS	426	15.610	35.376	0.531	1.00	25.12
ATOM	1759	CG	LYS	426	15.150	36.115	1.775	1.00	28.49
ATOM	1760	CD	LYS	426	14.489	37.445	1.415	1.00	29.27
ATOM	1761	CE	LYS	426	13.995	38.148	2.666	1.00	32.12
ATOM	1762	NZ	LYS	426	13.235	39.411	2.390	1.00	31.15
ATOM	1763	C	LYS	426	15.083	34.497	-1.733	1.00	25.06
ATOM	1764	O	LYS	426	15.363	35.209	-2.703	1.00	24.27
ATOM	1765	N	LEU	427	15.278	33.183	-1.717	1.00	25.20
ATOM	1766	CA	LEU	427	15.848	32.480	-2.857	1.00	26.06
ATOM	1767	CB	LEU	427	16.165	31.032	-2.473	1.00	25.95
ATOM	1768	CG	LEU	427	16.582	30.058	-3.581	1.00	27.66
ATOM	1769	CD1	LEU	427	17.718	30.638	-4.415	1.00	26.38
ATOM	1770	CD2	LEU	427	17.002	28.740	-2.940	1.00	27.07
ATOM	1771	C	LEU	427	14.922	32.523	-4.072	1.00	26.54
ATOM	1772	O	LEU	427	15.383	32.716	-5.194	1.00	26.46
ATOM	1773	N	GLN	428	13.622	32.369	-3.847	1.00	27.45
ATOM	1774	CA	GLN	428	12.653	32.399	-4.942	1.00	29.19
ATOM	1775	CB	GLN	428	11.247	32.108	-4.416	1.00	32.05
ATOM	1776	CG	GLN	428	11.172	30.852	-3.561	1.00	36.92
ATOM	1777	CD	GLN	428	12.009	29.714	-4.139	1.00	39.47
ATOM	1778	OE1	GLN	428	11.946	29.442	-5.345	1.00	41.41
ATOM	1779	NE2	GLN	428	12.788	29.034	-3.281	1.00	37.83
ATOM	1780	C	GLN	428	12.654	33.736	-5.675	1.00	28.90
ATOM	1781	O	GLN	428	12.466	33.780	-6.889	1.00	28.50
ATOM	1782	N	VAL	429	12.844	34.826	-4.938	1.00	28.63
ATOM	1783	CA	VAL	429	12.893	36.145	-5.551	1.00	29.18
ATOM	1784	CB	VAL	429	12.708	37.272	-4.515	1.00	29.49
ATOM	1785	CG1	VAL	429	12.789	38.632	-5.215	1.00	30.49
ATOM	1786	CG2	VAL	429	11.362	37.126	-3.824	1.00	30.87
ATOM	1787	C	VAL	429	14.260	36.297	-6.210	1.00	28.70
ATOM	1788	O	VAL	429	14.398	36.924	-7.267	1.00	27.69
ATOM	1789	N	PHE	430	15.279	35.723	-5.584	1.00	28.04
ATOM	1790	CA	PHE	430	16.601	35.793	-6.177	1.00	28.41
ATOM	1791	CB	PHE	430	17.633	35.074	-5.317	1.00	27.09
ATOM	1792	CG	PHE	430	19.021	35.157	-5.872	1.00	27.44
ATOM	1793	CD1	PHE	430	19.777	36.314	-5.711	1.00	27.34
ATOM	1794	CD2	PHE	430	19.553	34.096	-6.602	1.00	26.42
ATOM	1795	CE1	PHE	430	21.049	36.415	-6.274	1.00	27.80
ATOM	1796	CE2	PHE	430	20.807	34.182	-7.166	1.00	27.06
ATOM	1797	CZ	PHE	430	21.564	35.346	-7.004	1.00	27.26
ATOM	1798	C	PHE	430	16.549	35.120	-7.553	1.00	28.91
ATOM	1799	O	PHE	430	17.104	35.641	-8.524	1.00	28.87
ATOM	1800	N	LYS	431	15.886	33.964	-7.622	1.00	29.85
ATOM	1801	CA	LYS	431	15.766	33.212	-8.874	1.00	32.68
ATOM	1802	CB	LYS	431	14.976	31.906	-8.670	1.00	33.56
ATOM	1803	CG	LYS	431	14.832	31.090	-9.970	1.00	37.44
ATOM	1804	CD	LYS	431	13.617	30.145	-9.977	1.00	39.34
ATOM	1805	CE	LYS	431	13.997	28.714	-9.618	1.00	41.84
ATOM	1806	NZ	LYS	431	14.937	28.127	-10.621	1.00	42.78
ATOM	1807	C	LYS	431	15.077	34.053	-9.944	1.00	33.57
ATOM	1808	O	LYS	431	15.415	33.958	-11.125	1.00	33.07
ATOM	1809	N	GLN	432	14.103	34.865	-9.536	1.00	34.34
ATOM	1810	CA	GLN	432	13.392	35.728	-10.484	1.00	35.91
ATOM	1811	CB	GLN	432	12.353	36.589	-9.768	1.00	38.08
ATOM	1812	CG	GLN	432	11.091	35.901	-9.303	1.00	39.88
ATOM	1813	CD	GLN	432	10.123	36.910	-8.684	1.00	41.50
ATOM	1814	OE1	GLN	432	10.388	37.471	-7.617	1.00	40.92
ATOM	1815	NE2	GLN	432	9.011	37.170	-9.372	1.00	42.35
ATOM	1816	C	GLN	432	14.362	36.676	-11.182	1.00	35.12
ATOM	1817	O	GLN	432	14.358	36.804	-12.408	1.00	35.26
ATOM	1818	N	SER	433	15.180	37.347	-10.377	1.00	34.32
ATOM	1819	CA	SER	433	16.156	38.313	-10.868	1.00	34.30
ATOM	1820	CB	SER	433	16.608	39.220	-9.718	1.00	33.92
ATOM	1821	OG	SER	433	15.605	40.165	-9.392	1.00	35.35
ATOM	1822	C	SER	433	17.386	37.707	-11.536	1.00	33.58
ATOM	1823	O	SER	433	17.948	38.298	-12.458	1.00	33.32
ATOM	1824	N	HIS	434	17.809	36.537	-11.071	1.00	33.33
ATOM	1825	CA	HIS	434	18.990	35.890	-11.635	1.00	34.01
ATOM	1826	CB	HIS	434	20.184	36.077	-10.697	1.00	34.09
ATOM	1827	CG	HIS	434	20.418	37.498	-10.299	1.00	34.93
ATOM	1828	CD2	HIS	434	21.195	38.462	-10.849	1.00	35.03
ATOM	1829	ND1	HIS	434	19.776	38.087	-9.232	1.00	35.41
ATOM	1830	CE1	HIS	434	20.147	39.351	-9.140	1.00	35.21
ATOM	1831	NE2	HIS	434	21.007	39.604	-10.110	1.00	36.62
ATOM	1832	C	HIS	434	18.771	34.405	-11.883	1.00	34.38
ATOM	1833	O	HIS	434	19.341	33.561	-11.193	1.00	33.93
ATOM	1834	N	PRO	435	17.938	34.064	-12.876	1.00	34.98

ATOM	1835	CD	PRO	435	17.182	34.919	-13.805	1.00	35.01
ATOM	1836	CA	PRO	435	17.689	32.650	-13.158	1.00	35.44
ATOM	1837	CB	PRO	435	16.607	32.695	-14.237	1.00	35.29
ATOM	1838	CG	PRO	435	16.916	33.963	-14.962	1.00	35.40
ATOM	1839	C	PRO	435	18.915	31.882	-13.613	1.00	36.20
ATOM	1840	O	PRO	435	19.122	30.758	-13.172	1.00	35.55
ATOM	1841	N	ASP	436	19.733	32.480	-14.481	1.00	37.54
ATOM	1842	CA	ASP	436	20.919	31.785	-14.980	1.00	40.08
ATOM	1843	CB	ASP	436	21.634	32.607	-16.058	1.00	42.72
ATOM	1844	CG	ASP	436	22.700	31.794	-16.803	1.00	45.95
ATOM	1845	OD1	ASP	436	22.313	30.821	-17.497	1.00	46.29
ATOM	1846	OD2	ASP	436	23.914	32.119	-16.695	1.00	47.67
ATOM	1847	C	ASP	436	21.918	31.423	-13.886	1.00	39.77
ATOM	1848	O	ASP	436	22.572	30.385	-13.966	1.00	39.96
ATOM	1849	N	ILE	437	22.042	32.270	-12.867	1.00	39.31
ATOM	1850	CA	ILE	437	22.972	31.999	-11.775	1.00	38.61
ATOM	1851	CB	ILE	437	23.096	33.227	-10.806	1.00	39.13
ATOM	1852	CG2	ILE	437	23.864	32.842	-9.547	1.00	39.06
ATOM	1853	CG1	ILE	437	23.848	34.378	-11.491	1.00	39.49
ATOM	1854	CD1	ILE	437	23.124	34.982	-12.681	1.00	41.59
ATOM	1855	C	ILE	437	22.538	30.757	-10.995	1.00	38.28
ATOM	1856	O	ILE	437	23.350	29.858	-10.745	1.00	37.65
ATOM	1857	N	VAL	438	21.255	30.692	-10.641	1.00	37.18
ATOM	1858	CA	VAL	438	20.727	29.566	-9.885	1.00	37.56
ATOM	1859	CB	VAL	438	19.239	29.785	-9.458	1.00	37.27
ATOM	1860	CG1	VAL	438	18.716	28.546	-8.751	1.00	36.25
ATOM	1861	CG2	VAL	438	19.116	30.983	-8.525	1.00	36.28
ATOM	1862	C	VAL	438	20.800	28.261	-10.672	1.00	38.30
ATOM	1863	O	VAL	438	21.265	27.246	-10.157	1.00	37.66
ATOM	1864	N	ASN	439	20.368	28.287	-11.927	1.00	39.10
ATOM	1865	CA	ASN	439	20.370	27.060	-12.716	1.00	39.91
ATOM	1866	CB	ASN	439	19.390	27.189	-13.895	1.00	41.62
ATOM	1867	CG	ASN	439	17.934	27.190	-13.445	1.00	43.36
ATOM	1868	OD1	ASN	439	17.596	26.609	-12.410	1.00	44.58
ATOM	1869	ND2	ASN	439	17.064	27.827	-14.225	1.00	44.62
ATOM	1870	C	ASN	439	21.711	26.555	-13.219	1.00	39.39
ATOM	1871	O	ASN	439	21.835	25.377	-13.561	1.00	40.93
ATOM	1872	N	THR	440	22.728	27.406	-13.260	1.00	39.19
ATOM	1873	CA	THR	440	24.017	26.950	-13.777	1.00	38.65
ATOM	1874	CB	THR	440	24.287	27.533	-15.181	1.00	38.77
ATOM	1875	OG1	THR	440	24.895	28.828	-15.057	1.00	40.00
ATOM	1876	CG2	THR	440	22.985	27.670	-15.955	1.00	38.78
ATOM	1877	C	THR	440	25.248	27.238	-12.926	1.00	37.59
ATOM	1878	O	THR	440	26.353	26.835	-13.290	1.00	38.22
ATOM	1879	N	LEU	441	25.079	27.940	-11.811	1.00	35.62
ATOM	1880	CA	LEU	441	26.224	28.254	-10.965	1.00	33.88
ATOM	1881	CB	LEU	441	26.494	29.762	-10.971	1.00	35.57
ATOM	1882	CG	LEU	441	27.001	30.326	-12.304	1.00	37.86
ATOM	1883	CD1	LEU	441	27.177	31.837	-12.174	1.00	38.20
ATOM	1884	CD2	LEU	441	28.321	29.677	-12.683	1.00	38.80
ATOM	1885	C	LEU	441	26.071	27.763	-9.533	1.00	31.60
ATOM	1886	O	LEU	441	27.064	27.532	-8.839	1.00	32.48
ATOM	1887	N	PHE	442	24.831	27.602	-9.086	1.00	28.10
ATOM	1888	CA	PHE	442	24.587	27.122	-7.731	1.00	25.29
ATOM	1889	CB	PHE	442	23.135	27.405	-7.318	1.00	25.99
ATOM	1890	CG	PHE	442	22.909	28.776	-6.747	1.00	27.30
ATOM	1891	CD1	PHE	442	23.833	29.796	-6.937	1.00	26.54
ATOM	1892	CD2	PHE	442	21.748	29.047	-6.026	1.00	27.97
ATOM	1893	CE1	PHE	442	23.604	31.064	-6.416	1.00	29.09
ATOM	1894	CE2	PHE	442	21.508	30.321	-5.499	1.00	28.50
ATOM	1895	CZ	PHE	442	22.438	31.326	-5.695	1.00	27.97
ATOM	1896	C	PHE	442	24.830	25.615	-7.676	1.00	23.49
ATOM	1897	O	PHE	442	24.616	24.907	-8.663	1.00	21.57
ATOM	1898	N	PRO	443	25.300	25.107	-6.525	1.00	21.70
ATOM	1899	CD	PRO	443	25.758	25.819	-5.316	1.00	21.76
ATOM	1900	CA	PRO	443	25.539	23.665	-6.414	1.00	21.30
ATOM	1901	CB	PRO	443	25.886	23.488	-4.940	1.00	20.81
ATOM	1902	CG	PRO	443	26.615	24.773	-4.619	1.00	20.63
ATOM	1903	C	PRO	443	24.263	22.911	-6.795	1.00	22.58
ATOM	1904	O	PRO	443	23.179	23.243	-6.326	1.00	21.97
ATOM	1905	N	PRO	444	24.377	21.893	-7.662	1.00	24.17
ATOM	1906	CD	PRO	444	25.574	21.463	-8.404	1.00	24.11
ATOM	1907	CA	PRO	444	23.205	21.117	-8.080	1.00	24.81
ATOM	1908	CB	PRO	444	23.825	19.970	-8.867	1.00	25.10
ATOM	1909	CG	PRO	444	24.976	20.652	-9.543	1.00	25.51
ATOM	1910	C	PRO	444	22.313	20.637	-6.933	1.00	24.27
ATOM	1911	O	PRO	444	21.093	20.599	-7.081	1.00	24.40
ATOM	1912	N	LEU	445	22.905	20.272	-5.797	1.00	23.78
ATOM	1913	CA	LEU	445	22.106	19.807	-4.653	1.00	23.55
ATOM	1914	CB	LEU	445	23.001	19.218	-3.563	1.00	22.47
ATOM	1915	CG	LEU	445	22.273	18.815	-2.274	1.00	21.23
ATOM	1916	CD1	LEU	445	21.251	17.742	-2.592	1.00	22.32
ATOM	1917	CD2	LEU	445	23.273	18.307	-1.242	1.00	20.86
ATOM	1918	C	LEU	445	21.278	20.943	-4.055	1.00	22.92
ATOM	1919	O	LEU	445	20.124	20.757	-3.647	1.00	21.21
ATOM	1920	N	TYR	446	21.880	22.121	-3.998	1.00	23.10

ATOM	1921	CA	TYR	446	21.197	23.284	-3.465	1.00	23.29
ATOM	1922	CB	TYR	446	22.171	24.458	-3.418	1.00	23.30
ATOM	1923	CG	TYR	446	21.611	25.737	-2.846	1.00	23.78
ATOM	1924	CD1	TYR	446	20.891	26.617	-3.647	1.00	25.71
ATOM	1925	CE1	TYR	446	20.430	27.835	-3.151	1.00	25.93
ATOM	1926	CD2	TYR	446	21.850	26.094	-1.518	1.00	23.35
ATOM	1927	CE2	TYR	446	21.394	27.311	-1.002	1.00	25.61
ATOM	1928	CZ	TYR	446	20.688	28.179	-1.829	1.00	26.53
ATOM	1929	OH	TYR	446	20.281	29.404	-1.359	1.00	26.63
ATOM	1930	C	TYR	446	19.986	23.592	-4.346	1.00	25.01
ATOM	1931	O	TYR	446	18.903	23.896	-3.837	1.00	26.28
ATOM	1932	N	LYS	447	20.163	23.502	-5.664	1.00	24.54
ATOM	1933	CA	LYS	447	19.063	23.753	-6.591	1.00	26.44
ATOM	1934	CB	LYS	447	19.566	23.733	-8.042	1.00	28.07
ATOM	1935	CG	LYS	447	18.458	23.840	-9.086	1.00	33.16
ATOM	1936	CD	LYS	447	19.029	23.787	-10.514	1.00	36.54
ATOM	1937	CE	LYS	447	17.920	23.595	-11.542	1.00	39.14
ATOM	1938	NZ	LYS	447	18.494	23.447	-12.910	1.00	40.17
ATOM	1939	C	LYS	447	17.985	22.680	-6.414	1.00	25.88
ATOM	1940	O	LYS	447	16.796	22.980	-6.367	1.00	26.47
ATOM	1941	N	GLU	448	18.417	21.430	-6.306	1.00	25.85
ATOM	1942	CA	GLU	448	17.498	20.305	-6.147	1.00	26.71
ATOM	1943	CB	GLU	448	18.290	18.993	-6.099	1.00	26.95
ATOM	1944	CG	GLU	448	17.448	17.775	-5.804	1.00	29.45
ATOM	1945	CD	GLU	448	18.239	16.475	-5.861	1.00	29.93
ATOM	1946	OE1	GLU	448	18.785	16.140	-6.935	1.00	30.55
ATOM	1947	OE2	GLU	448	18.301	15.773	-4.832	1.00	30.84
ATOM	1948	C	GLU	448	16.637	20.432	-4.894	1.00	26.51
ATOM	1949	O	GLU	448	15.430	20.187	-4.923	1.00	26.27
ATOM	1950	N	LEU	449	17.268	20.832	-3.798	1.00	25.93
ATOM	1951	CA	LEU	449	16.589	20.981	-2.523	1.00	26.71
ATOM	1952	CB	LEU	449	17.622	21.017	-1.392	1.00	26.21
ATOM	1953	CG	LEU	449	18.502	19.788	-1.172	1.00	26.61
ATOM	1954	CD1	LEU	449	19.610	20.112	-0.154	1.00	25.71
ATOM	1955	CD2	LEU	449	17.633	18.623	-0.697	1.00	26.71
ATOM	1956	C	LEU	449	15.674	22.189	-2.364	1.00	28.16
ATOM	1957	O	LEU	449	14.593	22.064	-1.782	1.00	28.09
ATOM	1958	N	PHE	450	16.098	23.348	-2.876	1.00	29.00
ATOM	1959	CA	PHE	450	15.338	24.577	-2.692	1.00	31.20
ATOM	1960	CB	PHE	450	16.224	25.609	-1.993	1.00	29.89
ATOM	1961	CG	PHE	450	16.886	25.084	-0.757	1.00	27.85
ATOM	1962	CD1	PHE	450	18.263	24.862	-0.729	1.00	27.95
ATOM	1963	CD2	PHE	450	16.127	24.748	0.362	1.00	28.29
ATOM	1964	CE1	PHE	450	18.877	24.305	0.402	1.00	27.72
ATOM	1965	CE2	PHE	450	16.723	24.190	1.498	1.00	27.38
ATOM	1966	CZ	PHE	450	18.105	23.966	1.518	1.00	28.09
ATOM	1967	C	PHE	450	14.625	25.257	-3.854	1.00	33.41
ATOM	1968	O	PHE	450	13.844	26.169	-3.615	1.00	32.89
ATOM	1969	N	ASN	451	14.889	24.862	-5.096	1.00	36.22
ATOM	1970	CA	ASN	451	14.185	25.493	-6.219	1.00	39.47
ATOM	1971	CB	ASN	451	15.168	26.004	-7.281	1.00	41.40
ATOM	1972	CG	ASN	451	15.939	27.245	-6.818	1.00	43.69
ATOM	1973	OD1	ASN	451	15.371	28.342	-6.672	1.00	44.14
ATOM	1974	ND2	ASN	451	17.238	27.071	-6.567	1.00	44.76
ATOM	1975	C	ASN	451	13.217	24.509	-6.851	1.00	40.32
ATOM	1976	O	ASN	451	11.993	24.725	-6.697	1.00	41.43
ATOM	1977	OXT	ASN	451	13.696	23.537	-7.475	1.00	40.86
ATOM	1978	CB	HIS	691	15.393	13.885	-4.499	1.00	41.85
ATOM	1979	CG	HIS	691	13.918	14.001	-4.283	1.00	43.67
ATOM	1980	CD2	HIS	691	13.151	15.051	-3.912	1.00	44.45
ATOM	1981	ND1	HIS	691	13.051	12.954	-4.521	1.00	44.92
ATOM	1982	CE1	HIS	691	11.810	13.358	-4.305	1.00	45.35
ATOM	1983	NE2	HIS	691	11.843	14.625	-3.935	1.00	45.49
ATOM	1984	C	HIS	691	16.996	13.164	-6.244	1.00	38.01
ATOM	1985	O	HIS	691	17.471	12.469	-5.361	1.00	38.13
ATOM	1986	N	HIS	691	14.685	13.691	-6.864	1.00	39.52
ATOM	1987	CA	HIS	691	15.813	14.063	-5.956	1.00	39.14
ATOM	1988	N	LYS	692	17.475	13.190	-7.484	1.00	36.76
ATOM	1989	CA	LYS	692	18.589	12.350	-7.903	1.00	35.59
ATOM	1990	CB	LYS	692	18.893	12.623	-9.378	1.00	37.83
ATOM	1991	CG	LYS	692	19.742	11.564	-10.051	1.00	40.63
ATOM	1992	CD	LYS	692	19.728	11.714	-11.575	1.00	42.76
ATOM	1993	CE	LYS	692	20.323	10.472	-12.235	1.00	43.47
ATOM	1994	NZ	LYS	692	21.706	10.196	-11.753	1.00	43.90
ATOM	1995	C	LYS	692	19.873	12.498	-7.080	1.00	33.87
ATOM	1996	O	LYS	692	20.467	11.509	-6.658	1.00	33.35
ATOM	1997	N	ILE	693	20.309	13.729	-6.857	1.00	32.23
ATOM	1998	CA	ILE	693	21.535	13.950	-6.113	1.00	31.32
ATOM	1999	CB	ILE	693	21.930	15.427	-6.149	1.00	30.80
ATOM	2000	CG2	ILE	693	23.269	15.635	-5.440	1.00	29.72
ATOM	2001	CG1	ILE	693	22.033	15.873	-7.608	1.00	31.13
ATOM	2002	CD1	ILE	693	22.234	17.371	-7.780	1.00	31.56
ATOM	2003	C	ILE	693	21.432	13.482	-4.678	1.00	30.60
ATOM	2004	O	ILE	693	22.298	12.750	-4.201	1.00	30.47
ATOM	2005	N	LEU	694	20.373	13.894	-3.988	1.00	30.60
ATOM	2006	CA	LEU	694	20.189	13.498	-2.599	1.00	29.95

ATOM	2007	CB	LEU	694	18.901	14.127	-2.049	1.00	30.02
ATOM	2008	CG	LEU	694	18.575	13.956	-0.565	1.00	30.42
ATOM	2009	CD1	LEU	694	19.761	14.380	0.289	1.00	27.83
ATOM	2010	CD2	LEU	694	17.338	14.782	-0.228	1.00	29.11
ATOM	2011	C	LEU	694	20.133	11.973	-2.530	1.00	31.03
ATOM	2012	O	LEU	694	20.692	11.347	-1.624	1.00	28.47
ATOM	2013	N	HIS	695	19.476	11.365	-3.512	1.00	31.88
ATOM	2014	CA	HIS	695	19.374	9.913	-3.529	1.00	33.30
ATOM	2015	CB	HIS	695	18.477	9.459	-4.670	1.00	36.30
ATOM	2016	CG	HIS	695	17.945	8.080	-4.478	1.00	40.00
ATOM	2017	CD2	HIS	695	16.683	7.629	-4.299	1.00	41.54
ATOM	2018	ND1	HIS	695	18.768	6.980	-4.364	1.00	41.93
ATOM	2019	CE1	HIS	695	18.035	5.910	-4.117	1.00	42.57
ATOM	2020	NE2	HIS	695	16.766	6.277	-4.071	1.00	43.22
ATOM	2021	C	HIS	695	20.746	9.260	-3.676	1.00	33.11
ATOM	2022	O	HIS	695	21.048	8.249	-3.040	1.00	32.39
ATOM	2023	N	ARG	696	21.579	9.849	-4.521	1.00	32.29
ATOM	2024	CA	ARG	696	22.909	9.322	-4.743	1.00	30.93
ATOM	2025	CB	ARG	696	23.603	10.093	-5.867	1.00	31.23
ATOM	2026	CG	ARG	696	24.984	9.543	-6.182	1.00	32.75
ATOM	2027	CD	ARG	696	25.804	10.477	-7.050	1.00	33.56
ATOM	2028	NE	ARG	696	27.125	9.909	-7.307	1.00	35.72
ATOM	2029	CZ	ARG	696	28.099	10.546	-7.950	1.00	35.45
ATOM	2030	NH1	ARG	696	27.901	11.782	-8.398	1.00	35.32
ATOM	2031	NH2	ARG	696	29.268	9.943	-8.151	1.00	36.04
ATOM	2032	C	ARG	696	23.772	9.386	-3.480	1.00	29.89
ATOM	2033	O	ARG	696	24.475	8.433	-3.161	1.00	29.24
ATOM	2034	N	LEU	697	23.716	10.509	-2.768	1.00	29.17
ATOM	2035	CA	LEU	697	24.511	10.690	-1.557	1.00	28.52
ATOM	2036	CB	LEU	697	24.368	12.124	-1.046	1.00	26.92
ATOM	2037	CG	LEU	697	24.699	13.228	-2.053	1.00	27.27
ATOM	2038	CD1	LEU	697	24.463	14.602	-1.417	1.00	25.02
ATOM	2039	CD2	LEU	697	26.142	13.085	-2.505	1.00	26.53
ATOM	2040	C	LEU	697	24.140	9.712	-0.448	1.00	29.70
ATOM	2041	O	LEU	697	25.004	9.258	0.302	1.00	28.66
ATOM	2042	N	LEU	698	22.853	9.397	-0.345	1.00	31.41
ATOM	2043	CA	LEU	698	22.375	8.453	0.661	1.00	34.12
ATOM	2044	CB	LEU	698	20.846	8.472	0.718	1.00	33.23
ATOM	2045	CG	LEU	698	20.134	9.426	1.669	1.00	32.91
ATOM	2046	CD1	LEU	698	18.680	9.463	1.307	1.00	33.90
ATOM	2047	CD2	LEU	698	20.302	8.964	3.107	1.00	31.41
ATOM	2048	C	LEU	698	22.848	7.044	0.315	1.00	36.29
ATOM	2049	O	LEU	698	23.159	6.242	1.194	1.00	36.31
ATOM	2050	N	GLN	699	22.909	6.760	-0.977	1.00	39.15
ATOM	2051	CA	GLN	699	23.328	5.450	-1.471	1.00	42.12
ATOM	2052	CB	GLN	699	22.802	5.239	-2.896	1.00	43.64
ATOM	2053	CG	GLN	699	21.274	5.140	-2.989	1.00	45.98
ATOM	2054	CD	GLN	699	20.750	3.781	-2.547	1.00	47.08
ATOM	2055	OE1	GLN	699	21.233	3.204	-1.566	1.00	48.60
ATOM	2056	NE2	GLN	699	19.747	3.269	-3.258	1.00	48.36
ATOM	2057	C	GLN	699	24.836	5.245	-1.465	1.00	43.37
ATOM	2058	O	GLN	699	25.305	4.126	-1.660	1.00	43.65
ATOM	2059	N	GLU	700	25.599	6.312	-1.260	1.00	44.64
ATOM	2060	CA	GLU	700	27.052	6.190	-1.250	1.00	47.04
ATOM	2061	CB	GLU	700	27.700	7.568	-1.095	1.00	47.40
ATOM	2062	CG	GLU	700	29.220	7.519	-1.157	1.00	49.39
ATOM	2063	CD	GLU	700	29.791	8.048	-2.461	1.00	49.85
ATOM	2064	OE1	GLU	700	29.288	7.680	-3.554	1.00	49.19
ATOM	2065	OE2	GLU	700	30.763	8.836	-2.382	1.00	51.58
ATOM	2066	C	GLU	700	27.540	5.255	-0.132	1.00	48.52
ATOM	2067	O	GLU	700	28.449	4.423	-0.386	1.00	48.99
ATOM	2068	OXT	GLU	700	27.021	5.379	1.001	1.00	49.57
ATOM	2069	OH2	WAT	801	14.817	26.937	2.587	1.00	20.16
ATOM	2070	OH2	WAT	802	26.733	20.689	8.917	1.00	19.93
ATOM	2071	OH2	WAT	803	26.566	41.076	13.914	1.00	25.96
ATOM	2072	OH2	WAT	804	12.901	16.692	8.722	1.00	19.78
ATOM	2073	OH2	WAT	805	21.441	41.033	3.838	1.00	27.88
ATOM	2074	OH2	WAT	806	11.576	19.809	13.280	1.00	21.67
ATOM	2075	OH2	WAT	807	24.269	17.527	14.566	1.00	22.47
ATOM	2076	OH2	WAT	808	25.329	19.487	-5.550	1.00	38.43
ATOM	2077	OH2	WAT	809	28.090	41.701	1.977	1.00	27.58
ATOM	2078	OH2	WAT	810	1.405	9.268	4.014	1.00	28.13
ATOM	2079	OH2	WAT	811	7.275	28.248	11.748	1.00	33.78
ATOM	2080	OH2	WAT	812	24.068	26.427	23.332	1.00	29.89
ATOM	2081	OH2	WAT	813	14.772	34.264	14.684	1.00	25.08
ATOM	2082	OH2	WAT	814	12.543	3.741	17.005	1.00	29.72
ATOM	2083	OH2	WAT	815	30.580	18.289	2.261	1.00	31.66
ATOM	2084	OH2	WAT	816	36.688	39.061	2.238	1.00	31.61
ATOM	2085	OH2	WAT	817	11.630	23.199	6.840	1.00	31.07
ATOM	2086	OH2	WAT	818	2.742	5.405	10.288	1.00	30.11
ATOM	2087	OH2	WAT	819	1.368	13.915	5.083	1.00	35.24
ATOM	2088	OH2	WAT	820	3.546	13.308	8.739	1.00	32.87
ATOM	2089	OH2	WAT	821	0.197	11.314	7.692	1.00	31.34
ATOM	2090	OH2	WAT	822	-0.265	12.324	3.836	1.00	31.56
ATOM	2091	OH2	WAT	823	32.317	41.732	11.781	1.00	30.31
ATOM	2092	OH2	WAT	824	31.188	22.170	11.656	1.00	30.40

ATOM	2093	OH2	WAT	825	28.708	24.054	13.003	1.00	32.74
ATOM	2094	OH2	WAT	826	30.451	24.872	11.210	1.00	53.39
ATOM	2095	OH2	WAT	832	14.659	19.191	30.954	1.00	33.74
ATOM	2096	OH2	WAT	835	2.458	12.055	6.762	1.00	30.04
ATOM	2097	OH2	WAT	836	8.996	22.689	12.009	1.00	49.90
ATOM	2098	OH2	WAT	837	14.375	24.499	4.186	1.00	30.61
ATOM	2099	OH2	WAT	839	2.130	4.386	7.857	1.00	30.22
ATOM	2100	OH2	WAT	840	26.339	16.316	27.739	1.00	35.01
ATOM	2101	OH2	WAT	841	8.001	21.050	7.844	1.00	25.09
ATOM	2102	OH2	WAT	842	11.218	3.956	14.667	1.00	29.78
ATOM	2103	OH2	WAT	843	13.538	3.582	13.108	1.00	29.55
ATOM	2104	OH2	WAT	844	12.401	22.827	13.222	1.00	30.20
ATOM	2105	OH2	WAT	846	34.979	40.443	11.829	1.00	38.06
ATOM	2106	OH2	WAT	847	9.388	6.952	8.514	1.00	44.86
ATOM	2107	OH2	WAT	848	9.424	32.516	7.968	1.00	34.80
ATOM	2108	OH2	WAT	849	12.152	25.422	5.217	1.00	33.49
ATOM	2109	OH2	WAT	850	38.479	45.718	1.108	1.00	32.54
ATOM	2110	OH2	WAT	851	32.489	27.280	7.768	1.00	52.84
ATOM	2111	OH2	WAT	852	19.651	17.055	-9.301	1.00	37.88
ATOM	2112	OH2	WAT	853	18.746	43.921	3.425	1.00	36.94
ATOM	2113	OH2	WAT	854	25.431	10.057	28.150	1.00	38.06
ATOM	2114	OH2	WAT	855	7.134	18.540	4.931	1.00	63.81
ATOM	2115	OH2	WAT	856	9.614	18.288	18.085	1.00	35.99
ATOM	2116	OH2	WAT	857	9.960	11.674	24.894	1.00	34.82
ATOM	2117	OH2	WAT	858	21.673	44.846	2.726	1.00	29.09
ATOM	2118	OH2	WAT	859	12.420	-0.591	5.172	1.00	56.22
ATOM	2119	OH2	WAT	860	2.112	7.553	21.676	1.00	63.50
ATOM	2120	OH2	WAT	861	32.871	18.504	18.445	1.00	37.53
ATOM	2121	OH2	WAT	862	7.060	24.628	6.457	1.00	41.11
ATOM	2122	OH2	WAT	863	30.339	19.808	24.562	1.00	35.73
ATOM	2123	OH2	WAT	865	31.408	40.456	-6.981	1.00	28.87
ATOM	2124	OH2	WAT	866	16.060	42.941	9.793	1.00	44.24
ATOM	2125	OH2	WAT	867	12.843	26.219	0.918	1.00	35.68
ATOM	2126	OH2	WAT	868	37.364	44.144	-7.616	1.00	64.48
ATOM	2127	OH2	WAT	869	8.875	20.108	12.516	1.00	35.65
ATOM	2128	OH2	WAT	870	15.439	22.492	5.981	1.00	34.94
ATOM	2129	OH2	WAT	871	23.795	42.644	6.558	1.00	37.44
ATOM	2130	OH2	WAT	873	24.777	38.088	21.937	1.00	37.38
ATOM	2131	OH2	WAT	874	19.791	35.055	-15.004	1.00	49.00
ATOM	2132	OH2	WAT	875	4.885	20.278	10.170	1.00	42.95
ATOM	2133	OH2	WAT	876	22.387	24.643	-10.436	1.00	51.01
ATOM	2134	OH2	WAT	877	12.606	26.960	-1.579	1.00	38.28
ATOM	2135	OH2	WAT	878	29.020	8.186	21.464	1.00	34.65
ATOM	2136	OH2	WAT	879	19.154	5.255	15.898	1.00	45.06
ATOM	2137	OH2	WAT	880	23.704	47.324	18.452	1.00	68.34
ATOM	2138	OH2	WAT	881	28.057	9.062	6.603	1.00	44.32
ATOM	2139	OH2	WAT	883	43.023	41.890	5.788	1.00	38.31
ATOM	2140	OH2	WAT	884	7.119	28.891	9.099	1.00	32.09
ATOM	2141	OH2	WAT	885	17.021	2.408	2.764	1.00	45.47
ATOM	2142	OH2	WAT	886	23.215	4.005	10.105	1.00	32.13
ATOM	2143	OH2	WAT	887	15.983	38.039	-2.715	1.00	54.73
ATOM	2144	OH2	WAT	889	4.205	3.441	11.079	1.00	39.06
ATOM	2145	OH2	WAT	890	20.791	9.054	-7.915	1.00	33.22
ATOM	2146	OH2	WAT	891	25.305	7.602	26.964	1.00	51.43
ATOM	2147	OH2	WAT	892	27.413	6.919	14.503	1.00	32.31
ATOM	2148	OH2	WAT	893	33.552	15.908	12.742	1.00	47.40
ATOM	2149	OH2	WAT	894	27.172	23.883	29.442	1.00	51.19
ATOM	2150	OH2	WAT	895	32.219	29.350	18.302	1.00	39.52
ATOM	2151	OH2	WAT	896	20.082	1.162	10.052	1.00	37.15
ATOM	2152	OH2	WAT	898	23.983	4.384	5.989	1.00	35.18
ATOM	2153	OH2	WAT	899	9.782	19.780	0.976	1.00	50.23
ATOM	2154	OH2	WAT	900	36.407	19.082	20.876	1.00	44.97
ATOM	2155	OH2	WAT	901	7.403	19.567	14.815	1.00	37.37
ATOM	2156	OH2	WAT	902	39.710	36.772	1.207	1.00	58.27
ATOM	2157	OH2	WAT	903	10.185	18.360	15.457	1.00	33.56
ATOM	2158	OH2	WAT	904	10.260	38.244	11.664	1.00	51.98
ATOM	2159	OH2	WAT	905	11.584	31.849	-8.614	1.00	37.52
ATOM	2160	OH2	WAT	906	31.638	29.686	-0.266	1.00	32.48
ATOM	2161	OH2	WAT	907	-0.206	4.924	11.081	1.00	36.49
ATOM	2162	OH2	WAT	908	31.665	29.237	6.272	1.00	49.19
ATOM	2163	OH2	WAT	909	-2.417	16.800	9.041	1.00	44.02
ATOM	2164	OH2	WAT	910	10.940	39.261	6.571	1.00	43.92
ATOM	2165	OH2	WAT	911	13.036	1.866	1.304	1.00	40.13
ATOM	2166	OH2	WAT	912	14.565	2.593	15.801	1.00	47.21
ATOM	2167	OH2	WAT	913	15.968	17.289	31.561	1.00	33.25
ATOM	2168	OH2	WAT	914	34.332	36.096	17.436	1.00	48.32
ATOM	2169	OH2	WAT	915	-0.731	12.520	9.973	1.00	49.45
ATOM	2170	OH2	WAT	916	19.666	1.578	18.349	1.00	44.84
ATOM	2171	OH2	WAT	917	22.978	40.125	16.179	1.00	45.10
ATOM	2172	OH2	WAT	918	14.785	33.819	17.497	1.00	38.88
ATOM	2173	OH2	WAT	919	25.871	13.595	-7.644	1.00	45.77
ATOM	2174	OH2	WAT	920	25.570	6.591	-4.596	1.00	38.57
ATOM	2175	OH2	WAT	921	16.974	2.870	16.605	1.00	33.05
ATOM	2176	OH2	WAT	922	33.181	45.831	10.253	1.00	42.64
ATOM	2177	OH2	WAT	923	12.975	32.550	-12.651	1.00	46.09
ATOM	2178	OH2	WAT	924	26.965	45.895	0.183	1.00	55.12

ATOM	2179	OH2	WAT	925	7.626	22.836	18.961	1.00	41.09
ATOM	2180	OH2	WAT	926	23.414	34.472	23.517	1.00	34.89
ATOM	2181	OH2	WAT	927	21.725	53.855	-1.107	1.00	58.84
ATOM	2182	OH2	WAT	928	30.305	48.946	2.286	1.00	45.28
ATOM	2183	OH2	WAT	929	21.547	3.556	1.853	1.00	49.41
ATOM	2184	OH2	WAT	930	18.916	35.911	-17.290	1.00	54.56
ATOM	2185	OH2	WAT	931	7.922	23.555	24.917	1.00	41.77
ATOM	2186	OH2	WAT	932	22.938	41.070	21.176	1.00	38.69
ATOM	2187	OH2	WAT	933	34.983	42.284	-3.078	1.00	35.66
ATOM	2188	OH2	WAT	934	10.445	29.254	25.404	1.00	53.07
ATOM	2189	OH2	WAT	935	13.385	22.747	1.929	1.00	57.68
ATOM	2190	OH2	WAT	936	17.800	1.033	15.037	1.00	43.46
ATOM	2191	OH2	WAT	938	29.919	23.540	7.796	1.00	38.24
ATOM	2192	OH2	WAT	939	26.837	29.236	-6.134	1.00	34.00
ATOM	2193	OH2	WAT	940	4.282	1.689	8.958	1.00	44.18
ATOM	2194	OH2	WAT	941	16.572	41.825	-1.750	1.00	64.20
ATOM	2195	OH2	WAT	942	18.212	46.711	4.803	1.00	54.44
ATOM	2196	OH2	WAT	943	15.478	42.818	4.335	1.00	50.85
ATOM	2197	OH2	WAT	944	26.414	23.899	9.989	1.00	39.22
ATOM	2198	OH2	WAT	945	29.440	21.150	9.611	1.00	32.92
ATOM	2199	OH2	WAT	946	30.822	26.523	9.587	1.00	53.88
ATOM	2200	OH2	WAT	950	8.855	22.869	6.573	1.00	38.42
ATOM	2201	OH2	WAT	951	5.112	26.325	5.735	1.00	61.02
ATOM	2202	OH2	WAT	952	-0.889	10.066	5.523	1.00	36.76
ATOM	2203	OH2	WAT	954	34.805	28.111	7.254	1.00	38.30
ATOM	2204	OH2	WAT	955	19.872	20.234	-9.431	1.00	35.47
ATOM	2205	OH2	WAT	956	22.406	22.660	-11.886	1.00	39.93
ATOM	2206	O2	STE	1001	28.707	27.099	7.452	1.00	49.40
ATOM	2207	O1	STE	1001	27.940	25.317	8.529	1.00	50.77
ATOM	2208	C4	STE	1001	26.850	27.424	8.987	1.00	49.77
ATOM	2209	C1	STE	1001	25.793	30.578	5.434	1.00	50.35
ATOM	2210	C2	STE	1001	24.996	29.501	6.215	1.00	50.21
ATOM	2211	C6	STE	1001	25.841	28.419	6.860	1.00	50.29
ATOM	2212	C9	STE	1001	25.977	28.550	8.389	1.00	50.59
ATOM	2213	C5	STE	1001	23.387	34.488	6.590	1.00	48.06
ATOM	2214	C10	STE	1001	24.488	33.559	6.013	1.00	49.21
ATOM	2215	C13	STE	1001	25.128	32.598	7.006	1.00	49.62
ATOM	2216	C16	STE	1001	26.247	31.729	6.377	1.00	50.27
ATOM	2217	C7	STE	1001	20.503	31.145	6.873	1.00	45.75
ATOM	2218	C11	STE	1001	20.179	32.288	5.920	1.00	45.75
ATOM	2219	C14	STE	1001	21.350	33.208	5.604	1.00	46.43
ATOM	2220	C17	STE	1001	22.034	33.806	6.858	1.00	48.02
ATOM	2221	C8	STE	1001	20.032	29.801	6.378	1.00	44.03
ATOM	2222	C12	STE	1001	20.065	28.778	7.502	1.00	43.90
ATOM	2223	C15	STE	1001	21.407	28.027	7.586	1.00	42.74
ATOM	2224	C18	STE	1001	22.227	28.387	8.831	1.00	43.23
ATOM	2225	C3	STE	1001	27.878	26.507	8.311	1.00	50.33
END									

TABLE B: Crystallographic Coordinates of RORbeta LBD/retinoic acid/SRC1 peptide complex

ATOM	1	CB	THR	1	14.936	-1.893	26.570	1.00	44.08
ATOM	2	OG1	THR	1	16.329	-2.232	26.551	1.00	44.42
ATOM	3	CG2	THR	1	14.475	-1.471	25.180	1.00	44.84
ATOM	4	C	THR	1	15.825	0.265	27.508	1.00	44.25
ATOM	5	O	THR	1	16.183	0.740	26.428	1.00	42.75
ATOM	6	N	THR	1	13.347	-0.138	27.331	1.00	43.63
ATOM	7	CA	THR	1	14.685	-0.761	27.580	1.00	44.30
ATOM	8	N	MET	2	16.388	0.599	28.670	1.00	44.87
ATOM	9	CA	MET	2	17.474	1.576	28.770	1.00	45.02
ATOM	10	CB	MET	2	17.914	1.727	30.240	1.00	48.12
ATOM	11	CG	MET	2	18.864	2.913	30.535	1.00	52.67
ATOM	12	SD	MET	2	18.066	4.488	31.067	1.00	58.78
ATOM	13	CE	MET	2	18.185	4.360	32.887	1.00	53.72
ATOM	14	C	MET	2	18.669	1.176	27.894	1.00	43.49
ATOM	15	O	MET	2	19.405	2.034	27.406	1.00	42.50
ATOM	16	N	SER	3	18.854	-0.126	27.690	1.00	41.13
ATOM	17	CA	SER	3	19.955	-0.610	26.862	1.00	40.00
ATOM	18	CB	SER	3	19.927	-2.135	26.793	1.00	40.28
ATOM	19	OG	SER	3	20.891	-2.608	25.874	1.00	41.89
ATOM	20	C	SER	3	19.864	-0.031	25.447	1.00	38.47
ATOM	21	O	SER	3	20.860	0.429	24.883	1.00	37.74
ATOM	22	N	GLU	4	18.666	-0.056	24.876	1.00	36.43
ATOM	23	CA	GLU	4	18.464	0.478	23.536	1.00	34.72
ATOM	24	CB	GLU	4	17.076	0.100	23.003	1.00	34.35
ATOM	25	CG	GLU	4	16.711	0.808	21.697	1.00	35.50
ATOM	26	CD	GLU	4	15.384	0.347	21.124	1.00	36.78
ATOM	27	OE1	GLU	4	14.551	-0.177	21.896	1.00	38.95
ATOM	28	OE2	GLU	4	15.164	0.522	19.906	1.00	36.38
ATOM	29	C	GLU	4	18.624	1.995	23.536	1.00	33.23
ATOM	30	O	GLU	4	19.304	2.552	22.674	1.00	33.90

ATOM	31	N	ILE	5	18.010	2.661	24.511	1.00	31.72
ATOM	32	CA	ILE	5	18.099	4.112	24.600	1.00	30.77
ATOM	33	CB	ILE	5	17.390	4.654	25.856	1.00	31.04
ATOM	34	CG2	ILE	5	17.525	6.169	25.921	1.00	29.17
ATOM	35	CG1	ILE	5	15.907	4.272	25.828	1.00	31.73
ATOM	36	CD1	ILE	5	15.143	4.871	24.668	1.00	32.36
ATOM	37	C	ILE	5	19.554	4.547	24.640	1.00	30.75
ATOM	38	O	ILE	5	19.947	5.467	23.939	1.00	29.87
ATOM	39	N	ASP	6	20.358	3.876	25.458	1.00	31.69
ATOM	40	CA	ASP	6	21.769	4.227	25.567	1.00	31.78
ATOM	41	CB	ASP	6	22.433	3.437	26.706	1.00	35.48
ATOM	42	CG	ASP	6	23.900	3.807	26.898	1.00	37.43
ATOM	43	OD1	ASP	6	24.241	5.002	26.755	1.00	38.83
ATOM	44	OD2	ASP	6	24.711	2.907	27.203	1.00	39.59
ATOM	45	C	ASP	6	22.524	3.999	24.256	1.00	31.34
ATOM	46	O	ASP	6	23.303	4.855	23.832	1.00	30.34
ATOM	47	N	ARG	7	22.298	2.860	23.605	1.00	30.65
ATOM	48	CA	ARG	7	22.992	2.594	22.345	1.00	32.17
ATOM	49	CB	ARG	7	22.675	1.186	21.847	1.00	34.91
ATOM	50	CG	ARG	7	23.169	0.086	22.788	1.00	44.22
ATOM	51	CD	ARG	7	22.770	-1.289	22.276	1.00	48.39
ATOM	52	NE	ARG	7	21.346	-1.332	21.948	1.00	52.06
ATOM	53	CZ	ARG	7	20.751	-2.337	21.317	1.00	52.86
ATOM	54	NH1	ARG	7	21.456	-3.397	20.942	1.00	54.84
ATOM	55	NH2	ARG	7	19.454	-2.277	21.050	1.00	54.02
ATOM	56	C	ARG	7	22.620	3.631	21.280	1.00	30.15
ATOM	57	O	ARG	7	23.487	4.133	20.566	1.00	29.79
ATOM	58	N	ILE	8	21.332	3.954	21.185	1.00	28.75
ATOM	59	CA	ILE	8	20.865	4.944	20.220	1.00	27.58
ATOM	60	CB	ILE	8	19.330	5.161	20.324	1.00	26.92
ATOM	61	CG2	ILE	8	18.917	6.408	19.534	1.00	24.05
ATOM	62	CG1	ILE	8	18.589	3.924	19.803	1.00	28.50
ATOM	63	CD1	ILE	8	17.065	4.003	19.947	1.00	25.10
ATOM	64	C	ILE	8	21.571	6.271	20.494	1.00	28.49
ATOM	65	O	ILE	8	22.081	6.908	19.579	1.00	27.22
ATOM	66	N	ALA	9	21.600	6.677	21.760	1.00	28.38
ATOM	67	CA	ALA	9	22.241	7.929	22.147	1.00	28.28
ATOM	68	CB	ALA	9	22.086	8.150	23.648	1.00	26.41
ATOM	69	C	ALA	9	23.721	7.956	21.759	1.00	29.29
ATOM	70	O	ALA	9	24.176	8.890	21.099	1.00	27.81
ATOM	71	N	GLN	10	24.474	6.935	22.167	1.00	30.09
ATOM	72	CA	GLN	10	25.897	6.878	21.844	1.00	30.31
ATOM	73	CB	GLN	10	26.515	5.581	22.369	1.00	34.96
ATOM	74	CG	GLN	10	26.435	5.403	23.873	1.00	41.16
ATOM	75	CD	GLN	10	27.020	4.076	24.329	1.00	47.78
ATOM	76	OE1	GLN	10	28.217	3.809	24.162	1.00	48.59
ATOM	77	NE2	GLN	10	26.171	3.229	24.905	1.00	51.11
ATOM	78	C	GLN	10	26.141	6.967	20.338	1.00	28.54
ATOM	79	O	GLN	10	27.031	7.684	19.887	1.00	29.98
ATOM	80	N	ASN	11	25.350	6.228	19.568	1.00	26.39
ATOM	81	CA	ASN	11	25.486	6.216	18.115	1.00	25.48
ATOM	82	CB	ASN	11	24.439	5.266	17.524	1.00	25.98
ATOM	83	CG	ASN	11	24.439	5.251	16.014	1.00	24.40
ATOM	84	OD1	ASN	11	23.422	5.527	15.394	1.00	26.44
ATOM	85	ND2	ASN	11	25.578	4.920	15.413	1.00	24.88
ATOM	86	C	ASN	11	25.329	7.627	17.533	1.00	25.80
ATOM	87	O	ASN	11	26.106	8.047	16.674	1.00	25.13
ATOM	88	N	ILE	12	24.326	8.360	18.008	1.00	25.44
ATOM	89	CA	ILE	12	24.092	9.719	17.524	1.00	24.85
ATOM	90	CB	ILE	12	22.743	10.255	18.031	1.00	23.12
ATOM	91	CG2	ILE	12	22.617	11.739	17.719	1.00	22.76
ATOM	92	CG1	ILE	12	21.613	9.462	17.363	1.00	23.39
ATOM	93	CD1	ILE	12	20.253	9.769	17.882	1.00	20.56
ATOM	94	C	ILE	12	25.214	10.664	17.949	1.00	25.34
ATOM	95	O	ILE	12	25.683	11.474	17.158	1.00	25.18
ATOM	96	N	ILE	13	25.648	10.556	19.198	1.00	25.76
ATOM	97	CA	ILE	13	26.728	11.403	19.686	1.00	26.18
ATOM	98	CB	ILE	13	26.993	11.137	21.184	1.00	26.42
ATOM	99	CG2	ILE	13	28.317	11.759	21.605	1.00	27.88
ATOM	100	CG1	ILE	13	25.822	11.683	22.015	1.00	24.88
ATOM	101	CD1	ILE	13	25.887	11.341	23.510	1.00	24.90
ATOM	102	C	ILE	13	27.987	11.122	18.855	1.00	26.22
ATOM	103	O	ILE	13	28.680	12.045	18.423	1.00	25.36
ATOM	104	N	LYS	14	28.266	9.847	18.616	1.00	27.79
ATOM	105	CA	LYS	14	29.425	9.453	17.819	1.00	28.58
ATOM	106	CB	LYS	14	29.504	7.927	17.734	1.00	31.83
ATOM	107	CG	LYS	14	30.610	7.389	16.827	1.00	36.77
ATOM	108	CD	LYS	14	30.454	5.879	16.615	1.00	41.46
ATOM	109	CE	LYS	14	31.523	5.320	15.681	1.00	42.19
ATOM	110	NZ	LYS	14	32.877	5.449	16.278	1.00	44.14
ATOM	111	C	LYS	14	29.311	10.039	16.412	1.00	28.52

ATOM	112	O	LYS	14	30.268	10.609	15.883	1.00	29.83
ATOM	113	N	SER	15	28.136	9.905	15.806	1.00	26.79
ATOM	114	CA	SER	15	27.929	10.429	14.459	1.00	26.88
ATOM	115	CB	SER	15	26.500	10.132	13.994	1.00	27.05
ATOM	116	OG	SER	15	26.280	10.611	12.676	1.00	30.56
ATOM	117	C	SER	15	28.193	11.932	14.414	1.00	26.19
ATOM	118	O	SER	15	28.895	12.427	13.529	1.00	25.81
ATOM	119	N	HIS	16	27.627	12.657	15.373	1.00	25.25
ATOM	120	CA	HIS	16	27.807	14.104	15.448	1.00	25.35
ATOM	121	CB	HIS	16	27.098	14.652	16.688	1.00	23.98
ATOM	122	CG	HIS	16	27.485	16.055	17.035	1.00	22.83
ATOM	123	CD2	HIS	16	28.473	16.533	17.830	1.00	22.89
ATOM	124	ND1	HIS	16	26.831	17.159	16.530	1.00	21.54
ATOM	125	CE1	HIS	16	27.398	18.256	16.999	1.00	23.79
ATOM	126	NE2	HIS	16	28.398	17.904	17.789	1.00	24.95
ATOM	127	C	HIS	16	29.296	14.438	15.532	1.00	27.00
ATOM	128	O	HIS	16	29.794	15.325	14.832	1.00	25.20
ATOM	129	N	LEU	17	29.998	13.723	16.406	1.00	27.86
ATOM	130	CA	LEU	17	31.423	13.940	16.591	1.00	28.80
ATOM	131	CB	LEU	17	31.996	12.917	17.578	1.00	30.56
ATOM	132	CG	LEU	17	33.501	13.008	17.863	1.00	33.43
ATOM	133	CD1	LEU	17	33.784	14.232	18.725	1.00	35.11
ATOM	134	CD2	LEU	17	33.968	11.757	18.578	1.00	35.02
ATOM	135	C	LEU	17	32.153	13.809	15.269	1.00	28.50
ATOM	136	O	LEU	17	33.060	14.588	14.973	1.00	29.06
ATOM	137	N	GLU	18	31.758	12.833	14.466	1.00	27.38
ATOM	138	CA	GLU	18	32.430	12.584	13.197	1.00	29.19
ATOM	139	CB	GLU	18	32.419	11.080	12.897	1.00	30.86
ATOM	140	CG	GLU	18	32.740	10.192	14.093	1.00	35.14
ATOM	141	CD	GLU	18	32.508	8.718	13.807	1.00	38.27
ATOM	142	OE1	GLU	18	31.604	8.399	12.997	1.00	40.84
ATOM	143	OE2	GLU	18	33.215	7.877	14.407	1.00	38.21
ATOM	144	C	GLU	18	31.884	13.311	11.977	1.00	28.77
ATOM	145	O	GLU	18	32.495	13.242	10.909	1.00	29.35
ATOM	146	N	THR	19	30.767	14.023	12.109	1.00	26.26
ATOM	147	CA	THR	19	30.194	14.656	10.926	1.00	25.75
ATOM	148	CB	THR	19	28.916	13.921	10.510	1.00	24.77
ATOM	149	OG1	THR	19	27.906	14.120	11.508	1.00	22.37
ATOM	150	CG2	THR	19	29.194	12.428	10.366	1.00	24.32
ATOM	151	C	THR	19	29.888	16.148	10.903	1.00	26.21
ATOM	152	O	THR	19	29.143	16.606	10.040	1.00	26.97
ATOM	153	N	CYS	20	30.425	16.916	11.839	1.00	28.90
ATOM	154	CA	CYS	20	30.190	18.351	11.789	1.00	31.93
ATOM	155	CB	CYS	20	30.306	18.979	13.175	1.00	29.90
ATOM	156	SG	CYS	20	28.844	18.742	14.175	1.00	30.72
ATOM	157	C	CYS	20	31.258	18.930	10.876	1.00	33.01
ATOM	158	O	CYS	20	32.368	18.412	10.824	1.00	33.41
ATOM	159	N	GLN	21	30.927	19.986	10.143	1.00	34.90
ATOM	160	CA	GLN	21	31.911	20.595	9.261	1.00	36.25
ATOM	161	CB	GLN	21	31.314	21.782	8.509	1.00	37.23
ATOM	162	CG	GLN	21	32.359	22.563	7.731	1.00	39.86
ATOM	163	CD	GLN	21	31.797	23.770	7.024	1.00	39.83
ATOM	164	OE1	GLN	21	32.545	24.580	6.476	1.00	43.69
ATOM	165	NE2	GLN	21	30.478	23.900	7.025	1.00	41.69
ATOM	166	C	GLN	21	33.090	21.077	10.099	1.00	36.79
ATOM	167	O	GLN	21	34.229	21.077	9.636	1.00	36.87
ATOM	168	N	TYR	22	32.799	21.489	11.331	1.00	35.98
ATOM	169	CA	TYR	22	33.818	21.974	12.262	1.00	37.06
ATOM	170	CB	TYR	22	33.608	23.460	12.559	1.00	37.63
ATOM	171	CG	TYR	22	34.105	24.384	11.480	1.00	37.76
ATOM	172	CD1	TYR	22	35.467	24.505	11.219	1.00	39.21
ATOM	173	CE1	TYR	22	35.933	25.362	10.231	1.00	41.19
ATOM	174	CD2	TYR	22	33.217	25.142	10.724	1.00	38.25
ATOM	175	CE2	TYR	22	33.671	26.001	9.733	1.00	40.65
ATOM	176	CZ	TYR	22	35.029	26.105	9.492	1.00	40.42
ATOM	177	OH	TYR	22	35.483	26.946	8.509	1.00	43.37
ATOM	178	C	TYR	22	33.786	21.214	13.580	1.00	35.92
ATOM	179	O	TYR	22	32.767	21.199	14.268	1.00	35.59
ATOM	180	N	THR	23	34.900	20.587	13.935	1.00	36.10
ATOM	181	CA	THR	23	34.968	19.861	15.193	1.00	36.94
ATOM	182	CB	THR	23	36.179	18.921	15.242	1.00	39.58
ATOM	183	OG1	THR	23	37.380	19.700	15.216	1.00	39.59
ATOM	184	CG2	THR	23	36.169	17.969	14.056	1.00	40.40
ATOM	185	C	THR	23	35.128	20.892	16.302	1.00	36.49
ATOM	186	O	THR	23	35.459	22.052	16.041	1.00	32.29
ATOM	187	N	MET	24	34.895	20.471	17.539	1.00	37.33
ATOM	188	CA	MET	24	35.029	21.371	18.674	1.00	38.75
ATOM	189	CB	MET	24	34.654	20.648	19.966	1.00	39.75
ATOM	190	CG	MET	24	33.161	20.570	20.204	1.00	42.25
ATOM	191	SD	MET	24	32.471	22.130	20.821	1.00	43.80
ATOM	192	CE	MET	24	32.356	23.099	19.341	1.00	43.48

ATOM	193	C	MET	24	36.454	21.889	18.765	1.00	39.58
ATOM	194	O	MET	24	36.688	23.054	19.083	1.00	39.75
ATOM	195	N	GLU	25	37.409	21.017	18.469	1.00	41.04
ATOM	196	CA	GLU	25	38.808	21.397	18.529	1.00	41.50
ATOM	197	CB	GLU	25	39.685	20.172	18.242	1.00	45.13
ATOM	198	CG	GLU	25	39.356	18.989	19.165	1.00	50.86
ATOM	199	CD	GLU	25	40.586	18.370	19.829	1.00	55.72
ATOM	200	OE1	GLU	25	41.444	19.126	20.344	1.00	56.58
ATOM	201	OE2	GLU	25	40.686	17.122	19.851	1.00	57.47
ATOM	202	C	GLU	25	39.103	22.536	17.553	1.00	40.38
ATOM	203	O	GLU	25	39.708	23.538	17.928	1.00	37.53
ATOM	204	N	GLU	26	38.655	22.390	16.310	1.00	38.80
ATOM	205	CA	GLU	26	38.885	23.415	15.298	1.00	38.72
ATOM	206	CB	GLU	26	38.353	22.948	13.943	1.00	40.80
ATOM	207	CG	GLU	26	38.837	21.562	13.555	1.00	45.17
ATOM	208	CD	GLU	26	38.289	21.099	12.225	1.00	47.49
ATOM	209	OE1	GLU	26	37.059	21.191	12.023	1.00	50.42
ATOM	210	OE2	GLU	26	39.087	20.633	11.384	1.00	50.96
ATOM	211	C	GLU	26	38.205	24.716	15.701	1.00	37.74
ATOM	212	O	GLU	26	38.745	25.799	15.478	1.00	35.99
ATOM	213	N	LEU	27	37.020	24.604	16.298	1.00	37.47
ATOM	214	CA	LEU	27	36.278	25.776	16.744	1.00	37.81
ATOM	215	CB	LEU	27	34.894	25.369	17.272	1.00	36.85
ATOM	216	CG	LEU	27	33.650	25.542	16.379	1.00	36.21
ATOM	217	CD1	LEU	27	34.023	26.084	15.013	1.00	34.78
ATOM	218	CD2	LEU	27	32.927	24.214	16.248	1.00	34.77
ATOM	219	C	LEU	27	37.051	26.512	17.833	1.00	39.23
ATOM	220	O	LEU	27	37.145	27.738	17.820	1.00	37.29
ATOM	221	N	HIS	28	37.610	25.762	18.776	1.00	42.29
ATOM	222	CA	HIS	28	38.369	26.378	19.852	1.00	45.83
ATOM	223	CB	HIS	28	38.867	25.311	20.834	1.00	49.02
ATOM	224	CG	HIS	28	37.786	24.745	21.707	1.00	53.69
ATOM	225	CD2	HIS	28	36.461	25.024	21.782	1.00	54.33
ATOM	226	ND1	HIS	28	38.025	23.775	22.660	1.00	54.53
ATOM	227	CE1	HIS	28	36.896	23.484	23.283	1.00	53.92
ATOM	228	NE2	HIS	28	35.932	24.228	22.770	1.00	54.66
ATOM	229	C	HIS	28	39.533	27.202	19.306	1.00	46.70
ATOM	230	O	HIS	28	39.809	28.292	19.806	1.00	46.07
ATOM	231	N	GLN	29	40.206	26.695	18.277	1.00	47.88
ATOM	232	CA	GLN	29	41.321	27.432	17.686	1.00	49.79
ATOM	233	CB	GLN	29	42.205	26.504	16.841	1.00	51.23
ATOM	234	CG	GLN	29	43.142	25.629	17.673	1.00	55.35
ATOM	235	CD	GLN	29	42.632	24.210	17.843	1.00	57.34
ATOM	236	OE1	GLN	29	42.896	23.556	18.856	1.00	58.45
ATOM	237	NE2	GLN	29	41.913	23.717	16.839	1.00	58.43
ATOM	238	C	GLN	29	40.842	28.609	16.835	1.00	49.61
ATOM	239	O	GLN	29	41.532	29.621	16.725	1.00	50.02
ATOM	240	N	LEU	30	39.659	28.472	16.245	1.00	49.60
ATOM	241	CA	LEU	30	39.081	29.519	15.404	1.00	51.37
ATOM	242	CB	LEU	30	38.164	28.908	14.346	1.00	51.30
ATOM	243	CG	LEU	30	38.817	28.187	13.172	1.00	52.22
ATOM	244	CD1	LEU	30	37.770	27.391	12.407	1.00	51.55
ATOM	245	CD2	LEU	30	39.491	29.212	12.275	1.00	52.87
ATOM	246	C	LEU	30	38.266	30.493	16.233	1.00	52.89
ATOM	247	O	LEU	30	37.645	31.409	15.694	1.00	53.39
ATOM	248	N	ALA	31	38.271	30.283	17.544	1.00	54.40
ATOM	249	CA	ALA	31	37.509	31.107	18.474	1.00	54.90
ATOM	250	CB	ALA	31	37.875	30.728	19.902	1.00	55.70
ATOM	251	C	ALA	31	37.674	32.608	18.284	1.00	54.89
ATOM	252	O	ALA	31	36.695	33.339	18.109	1.00	52.72
ATOM	253	N	TRP	32	38.925	33.055	18.324	1.00	56.51
ATOM	254	CA	TRP	32	39.254	34.468	18.197	1.00	57.22
ATOM	255	CB	TRP	32	40.362	34.816	19.192	1.00	59.36
ATOM	256	CG	TRP	32	39.979	34.430	20.581	1.00	62.16
ATOM	257	CD2	TRP	32	39.717	35.315	21.678	1.00	63.50
ATOM	258	CE2	TRP	32	39.268	34.519	22.757	1.00	64.21
ATOM	259	CE3	TRP	32	39.814	36.702	21.855	1.00	63.45
ATOM	260	CD1	TRP	32	39.697	33.168	21.031	1.00	62.50
ATOM	261	NE1	TRP	32	39.265	33.215	22.335	1.00	63.94
ATOM	262	CZ2	TRP	32	38.913	35.068	23.995	1.00	63.81
ATOM	263	CZ3	TRP	32	39.461	37.244	23.087	1.00	62.65
ATOM	264	CH2	TRP	32	39.016	36.426	24.137	1.00	62.53
ATOM	265	C	TRP	32	39.667	34.850	16.787	1.00	57.28
ATOM	266	O	TRP	32	40.826	35.187	16.526	1.00	58.45
ATOM	267	N	GLN	33	38.701	34.802	15.879	1.00	54.65
ATOM	268	CA	GLN	33	38.954	35.145	14.494	1.00	52.60
ATOM	269	CB	GLN	33	39.326	33.892	13.697	1.00	54.99
ATOM	270	CG	GLN	33	40.753	33.411	13.884	1.00	59.00
ATOM	271	CD	GLN	33	41.772	34.297	13.184	1.00	61.62
ATOM	272	OE1	GLN	33	42.960	33.978	13.148	1.00	63.64
ATOM	273	NE2	GLN	33	41.312	35.415	12.624	1.00	63.55

ATOM	274	C	GLN	33	37.737	35.801	13.863	1.00	49.63
ATOM	275	O	GLN	33	36.785	35.124	13.489	1.00	47.22
ATOM	276	N	THR	34	37.763	37.125	13.771	1.00	47.47
ATOM	277	CA	THR	34	36.678	37.863	13.139	1.00	45.87
ATOM	278	CB	THR	34	36.159	39.019	14.033	1.00	46.83
ATOM	279	OG1	THR	34	37.237	39.911	14.346	1.00	46.09
ATOM	280	CG2	THR	34	35.556	38.475	15.321	1.00	47.41
ATOM	281	C	THR	34	37.269	38.446	11.856	1.00	44.40
ATOM	282	O	THR	34	38.469	38.731	11.797	1.00	44.57
ATOM	283	N	HIS	35	36.451	38.605	10.822	1.00	41.42
ATOM	284	CA	HIS	35	36.964	39.168	9.581	1.00	37.99
ATOM	285	CB	HIS	35	35.894	39.157	8.487	1.00	34.94
ATOM	286	CG	HIS	35	35.570	37.792	7.967	1.00	32.18
ATOM	287	CD2	HIS	35	36.167	37.037	7.015	1.00	30.88
ATOM	288	ND1	HIS	35	34.510	37.047	8.438	1.00	31.87
ATOM	289	CE1	HIS	35	34.467	35.893	7.797	1.00	30.43
ATOM	290	NE2	HIS	35	35.463	35.862	6.929	1.00	32.44
ATOM	291	C	HIS	35	37.414	40.601	9.844	1.00	36.88
ATOM	292	O	HIS	35	36.856	41.287	10.697	1.00	35.24
ATOM	293	N	THR	36	38.439	41.042	9.124	1.00	38.20
ATOM	294	CA	THR	36	38.949	42.402	9.276	1.00	39.26
ATOM	295	CB	THR	36	40.319	42.550	8.597	1.00	39.89
ATOM	296	OG1	THR	36	40.181	42.304	7.192	1.00	40.21
ATOM	297	CG2	THR	36	41.312	41.548	9.178	1.00	40.05
ATOM	298	C	THR	36	37.959	43.346	8.599	1.00	39.52
ATOM	299	O	THR	36	37.070	42.894	7.873	1.00	38.71
ATOM	300	N	TYR	37	38.101	44.648	8.824	1.00	40.48
ATOM	301	CA	TYR	37	37.186	45.595	8.197	1.00	41.59
ATOM	302	CB	TYR	37	37.474	47.026	8.653	1.00	44.12
ATOM	303	CG	TYR	37	37.124	47.289	10.099	1.00	46.75
ATOM	304	CD1	TYR	37	38.080	47.149	11.110	1.00	48.09
ATOM	305	CE1	TYR	37	37.754	47.392	12.453	1.00	49.23
ATOM	306	CD2	TYR	37	35.831	47.675	10.460	1.00	47.60
ATOM	307	CE2	TYR	37	35.493	47.916	11.795	1.00	49.16
ATOM	308	CZ	TYR	37	36.456	47.775	12.786	1.00	49.69
ATOM	309	OH	TYR	37	36.120	48.027	14.100	1.00	48.49
ATOM	310	C	TYR	37	37.269	45.515	6.678	1.00	41.21
ATOM	311	O	TYR	37	36.265	45.673	5.988	1.00	39.83
ATOM	312	N	GLU	38	38.469	45.270	6.158	1.00	40.73
ATOM	313	CA	GLU	38	38.652	45.161	4.715	1.00	41.99
ATOM	314	CB	GLU	38	40.136	45.020	4.358	1.00	43.80
ATOM	315	CG	GLU	38	40.985	46.242	4.668	1.00	46.95
ATOM	316	CD	GLU	38	41.266	46.412	6.154	1.00	48.29
ATOM	317	OE1	GLU	38	41.815	47.470	6.528	1.00	50.72
ATOM	318	OE2	GLU	38	40.948	45.493	6.943	1.00	48.78
ATOM	319	C	GLU	38	37.896	43.949	4.185	1.00	41.21
ATOM	320	O	GLU	38	37.284	44.000	3.122	1.00	39.46
ATOM	321	N	GLU	39	37.946	42.854	4.935	1.00	41.37
ATOM	322	CA	GLU	39	37.265	41.632	4.527	1.00	41.22
ATOM	323	CB	GLU	39	37.693	40.473	5.429	1.00	42.06
ATOM	324	CG	GLU	39	39.208	40.289	5.453	1.00	46.35
ATOM	325	CD	GLU	39	39.668	39.164	6.363	1.00	48.63
ATOM	326	OE1	GLU	39	39.234	39.126	7.534	1.00	48.96
ATOM	327	OE2	GLU	39	40.476	38.324	5.909	1.00	50.59
ATOM	328	C	GLU	39	35.756	41.844	4.581	1.00	39.62
ATOM	329	O	GLU	39	35.023	41.339	3.728	1.00	40.20
ATOM	330	N	ILE	40	35.296	42.601	5.575	1.00	37.13
ATOM	331	CA	ILE	40	33.873	42.885	5.706	1.00	36.49
ATOM	332	CB	ILE	40	33.541	43.587	7.058	1.00	35.15
ATOM	333	CG2	ILE	40	32.105	44.100	7.054	1.00	34.00
ATOM	334	CG1	ILE	40	33.715	42.603	8.219	1.00	34.57
ATOM	335	CD1	ILE	40	32.853	41.351	8.102	1.00	32.97
ATOM	336	C	ILE	40	33.445	43.784	4.557	1.00	36.47
ATOM	337	O	ILE	40	32.386	43.582	3.966	1.00	35.95
ATOM	338	N	LYS	41	34.277	44.772	4.233	1.00	37.54
ATOM	339	CA	LYS	41	33.955	45.688	3.141	1.00	38.47
ATOM	340	CB	LYS	41	35.023	46.774	3.002	1.00	41.50
ATOM	341	CG	LYS	41	34.532	48.021	2.277	1.00	45.40
ATOM	342	CD	LYS	41	33.917	49.022	3.257	1.00	49.51
ATOM	343	CE	LYS	41	32.816	48.394	4.110	1.00	50.14
ATOM	344	NZ	LYS	41	32.365	49.280	5.217	1.00	51.19
ATOM	345	C	LYS	41	33.876	44.899	1.846	1.00	36.39
ATOM	346	O	LYS	41	32.987	45.121	1.023	1.00	34.38
ATOM	347	N	ALA	42	34.813	43.972	1.679	1.00	35.77
ATOM	348	CA	ALA	42	34.855	43.134	0.492	1.00	36.18
ATOM	349	CB	ALA	42	35.999	42.132	0.599	1.00	37.07
ATOM	350	C	ALA	42	33.523	42.409	0.345	1.00	35.76
ATOM	351	O	ALA	42	32.958	42.355	-0.749	1.00	35.23
ATOM	352	N	TYR	43	33.015	41.868	1.451	1.00	34.54
ATOM	353	CA	TYR	43	31.740	41.155	1.423	1.00	33.59
ATOM	354	CB	TYR	43	31.423	40.539	2.794	1.00	33.00

ATOM	355	CG	TYR	43	32.175	39.263	3.093	1.00	31.41
ATOM	356	CD1	TYR	43	32.035	38.138	2.275	1.00	31.79
ATOM	357	CE1	TYR	43	32.734	36.959	2.543	1.00	32.00
ATOM	358	CD2	TYR	43	33.031	39.179	4.190	1.00	32.57
ATOM	359	CE2	TYR	43	33.735	38.006	4.468	1.00	32.13
ATOM	360	CZ	TYR	43	33.583	36.902	3.643	1.00	32.91
ATOM	361	OH	TYR	43	34.287	35.750	3.922	1.00	32.24
ATOM	362	C	TYR	43	30.589	42.061	1.017	1.00	33.94
ATOM	363	O	TYR	43	29.697	41.647	0.277	1.00	33.69
ATOM	364	N	GLN	44	30.605	43.295	1.510	1.00	34.41
ATOM	365	CA	GLN	44	29.540	44.244	1.206	1.00	35.55
ATOM	366	CB	GLN	44	29.571	45.405	2.210	1.00	36.41
ATOM	367	CG	GLN	44	29.489	44.944	3.665	1.00	38.05
ATOM	368	CD	GLN	44	29.509	46.090	4.667	1.00	39.51
ATOM	369	OE1	GLN	44	30.353	46.984	4.592	1.00	40.40
ATOM	370	NE2	GLN	44	28.588	46.056	5.621	1.00	38.09
ATOM	371	C	GLN	44	29.635	44.774	-0.220	1.00	35.22
ATOM	372	O	GLN	44	28.657	45.279	-0.769	1.00	35.57
ATOM	373	N	SER	45	30.813	44.645	-0.821	1.00	36.36
ATOM	374	CA	SER	45	31.029	45.115	-2.186	1.00	37.51
ATOM	375	CB	SER	45	32.490	45.520	-2.385	1.00	36.45
ATOM	376	OG	SER	45	32.830	46.585	-1.519	1.00	37.77
ATOM	377	C	SER	45	30.649	44.065	-3.224	1.00	37.52
ATOM	378	O	SER	45	30.433	44.390	-4.394	1.00	37.81
ATOM	379	N	LYS	46	30.581	42.805	-2.804	1.00	37.01
ATOM	380	CA	LYS	46	30.207	41.729	-3.718	1.00	37.49
ATOM	381	CB	LYS	46	30.185	40.385	-2.978	1.00	38.89
ATOM	382	CG	LYS	46	31.554	39.830	-2.619	1.00	41.39
ATOM	383	CD	LYS	46	32.285	39.347	-3.859	1.00	43.62
ATOM	384	CE	LYS	46	33.618	38.716	-3.501	1.00	45.39
ATOM	385	NZ	LYS	46	33.460	37.587	-2.542	1.00	46.78
ATOM	386	C	LYS	46	28.811	42.027	-4.261	1.00	36.47
ATOM	387	O	LYS	46	28.024	42.714	-3.616	1.00	34.79
ATOM	388	N	SER	47	28.505	41.526	-5.450	1.00	35.94
ATOM	389	CA	SER	47	27.181	41.741	-6.011	1.00	36.64
ATOM	390	CB	SER	47	27.149	41.341	-7.486	1.00	36.69
ATOM	391	OG	SER	47	27.443	39.964	-7.636	1.00	35.57
ATOM	392	C	SER	47	26.232	40.843	-5.225	1.00	37.24
ATOM	393	O	SER	47	26.672	39.994	-4.452	1.00	36.62
ATOM	394	N	ARG	48	24.934	41.026	-5.419	1.00	37.93
ATOM	395	CA	ARG	48	23.957	40.202	-4.726	1.00	37.32
ATOM	396	CB	ARG	48	22.551	40.762	-4.966	1.00	38.56
ATOM	397	CG	ARG	48	21.427	39.977	-4.315	1.00	38.73
ATOM	398	CD	ARG	48	20.311	40.908	-3.869	1.00	39.69
ATOM	399	NE	ARG	48	19.091	40.181	-3.530	1.00	41.75
ATOM	400	CZ	ARG	48	18.294	39.611	-4.429	1.00	43.27
ATOM	401	NH1	ARG	48	18.588	39.688	-5.721	1.00	43.91
ATOM	402	NH2	ARG	48	17.203	38.965	-4.041	1.00	41.76
ATOM	403	C	ARG	48	24.073	38.754	-5.220	1.00	36.87
ATOM	404	O	ARG	48	23.928	37.806	-4.441	1.00	35.81
ATOM	405	N	GLU	49	24.352	38.592	-6.511	1.00	34.76
ATOM	406	CA	GLU	49	24.501	37.268	-7.113	1.00	35.71
ATOM	407	CB	GLU	49	24.643	37.371	-8.636	1.00	38.45
ATOM	408	CG	GLU	49	23.676	38.328	-9.302	1.00	44.94
ATOM	409	CD	GLU	49	24.015	39.782	-9.028	1.00	47.01
ATOM	410	OE1	GLU	49	25.099	40.231	-9.460	1.00	49.86
ATOM	411	OE2	GLU	49	23.201	40.476	-8.380	1.00	46.92
ATOM	412	C	GLU	49	25.751	36.591	-6.568	1.00	33.86
ATOM	413	O	GLU	49	25.731	35.414	-6.213	1.00	33.86
ATOM	414	N	ALA	50	26.843	37.344	-6.511	1.00	32.28
ATOM	415	CA	ALA	50	28.098	36.804	-6.021	1.00	31.98
ATOM	416	CB	ALA	50	29.206	37.849	-6.139	1.00	30.17
ATOM	417	C	ALA	50	27.975	36.322	-4.579	1.00	31.48
ATOM	418	O	ALA	50	28.373	35.201	-4.263	1.00	29.44
ATOM	419	N	LEU	51	27.422	37.159	-3.703	1.00	30.98
ATOM	420	CA	LEU	51	27.289	36.762	-2.305	1.00	30.66
ATOM	421	CB	LEU	51	26.830	37.940	-1.441	1.00	30.32
ATOM	422	CG	LEU	51	26.893	37.675	0.070	1.00	32.08
ATOM	423	CD1	LEU	51	28.267	37.144	0.444	1.00	32.44
ATOM	424	CD2	LEU	51	26.594	38.952	0.842	1.00	32.02
ATOM	425	C	LEU	51	26.332	35.582	-2.156	1.00	29.32
ATOM	426	O	LEU	51	26.601	34.652	-1.393	1.00	28.16
ATOM	427	N	TRP	52	25.220	35.614	-2.886	1.00	28.73
ATOM	428	CA	TRP	52	24.261	34.520	-2.835	1.00	28.59
ATOM	429	CB	TRP	52	23.076	34.781	-3.770	1.00	30.93
ATOM	430	CG	TRP	52	21.878	35.296	-3.050	1.00	35.78
ATOM	431	CD2	TRP	52	20.905	34.513	-2.351	1.00	39.02
ATOM	432	CE2	TRP	52	19.993	35.413	-1.759	1.00	39.44
ATOM	433	CE3	TRP	52	20.720	33.135	-2.161	1.00	40.28
ATOM	434	CD1	TRP	52	21.524	36.602	-2.865	1.00	35.55
ATOM	435	NE1	TRP	52	20.391	36.681	-2.089	1.00	38.68

ATOM	436	CZ2	TRP	52	18.905	34.980	-0.991	1.00	42.34
ATOM	437	CZ3	TRP	52	19.644	32.705	-1.398	1.00	41.70
ATOM	438	CH2	TRP	52	18.749	33.626	-0.821	1.00	42.77
ATOM	439	C	TRP	52	24.929	33.213	-3.231	1.00	27.04
ATOM	440	O	TRP	52	24.704	32.182	-2.609	1.00	26.75
ATOM	441	N	GLN	53	25.742	33.259	-4.279	1.00	26.75
ATOM	442	CA	GLN	53	26.446	32.071	-4.740	1.00	27.50
ATOM	443	CB	GLN	53	27.209	32.391	-6.031	1.00	31.81
ATOM	444	CG	GLN	53	27.894	31.198	-6.678	1.00	36.92
ATOM	445	CD	GLN	53	28.277	31.456	-8.137	1.00	42.85
ATOM	446	OE1	GLN	53	28.893	30.609	-8.786	1.00	43.92
ATOM	447	NE2	GLN	53	27.904	32.628	-8.657	1.00	42.90
ATOM	448	C	GLN	53	27.403	31.558	-3.655	1.00	26.49
ATOM	449	O	GLN	53	27.530	30.354	-3.449	1.00	24.81
ATOM	450	N	GLN	54	28.071	32.473	-2.960	1.00	25.88
ATOM	451	CA	GLN	54	28.992	32.094	-1.890	1.00	27.32
ATOM	452	CB	GLN	54	29.727	33.323	-1.343	1.00	31.35
ATOM	453	CG	GLN	54	30.846	33.861	-2.229	1.00	37.27
ATOM	454	CD	GLN	54	31.493	35.112	-1.645	1.00	41.33
ATOM	455	OE1	GLN	54	31.105	36.239	-1.969	1.00	44.63
ATOM	456	NE2	GLN	54	32.474	34.916	-0.766	1.00	40.57
ATOM	457	C	GLN	54	28.210	31.445	-0.754	1.00	26.99
ATOM	458	O	GLN	54	28.621	30.423	-0.201	1.00	25.42
ATOM	459	N	CYS	55	27.084	32.060	-0.402	1.00	26.01
ATOM	460	CA	CYS	55	26.236	31.550	0.663	1.00	25.09
ATOM	461	CB	CYS	55	25.097	32.536	0.935	1.00	26.44
ATOM	462	SG	CYS	55	25.637	34.013	1.827	1.00	26.26
ATOM	463	C	CYS	55	25.673	30.175	0.304	1.00	24.90
ATOM	464	O	CYS	55	25.603	29.284	1.151	1.00	23.90
ATOM	465	N	ALA	56	25.287	30.011	-0.958	1.00	22.85
ATOM	466	CA	ALA	56	24.733	28.752	-1.438	1.00	22.57
ATOM	467	CB	ALA	56	24.310	28.903	-2.878	1.00	18.31
ATOM	468	C	ALA	56	25.765	27.625	-1.305	1.00	23.49
ATOM	469	O	ALA	56	25.425	26.499	-0.967	1.00	24.70
ATOM	470	N	ILE	57	27.027	27.937	-1.575	1.00	24.87
ATOM	471	CA	ILE	57	28.094	26.945	-1.471	1.00	26.21
ATOM	472	CB	ILE	57	29.390	27.479	-2.104	1.00	27.82
ATOM	473	CG2	ILE	57	30.597	26.671	-1.616	1.00	29.94
ATOM	474	CG1	ILE	57	29.260	27.432	-3.630	1.00	28.92
ATOM	475	CD1	ILE	57	30.484	27.913	-4.374	1.00	31.67
ATOM	476	C	ILE	57	28.348	26.554	-0.012	1.00	27.09
ATOM	477	O	ILE	57	28.465	25.370	0.306	1.00	27.29
ATOM	478	N	GLN	58	28.416	27.547	0.872	1.00	26.96
ATOM	479	CA	GLN	58	28.637	27.289	2.291	1.00	28.94
ATOM	480	CB	GLN	58	28.761	28.613	3.056	1.00	31.47
ATOM	481	CG	GLN	58	28.855	28.471	4.571	1.00	37.58
ATOM	482	CD	GLN	58	29.890	27.439	5.012	1.00	43.52
ATOM	483	OE1	GLN	58	31.043	27.458	4.557	1.00	45.14
ATOM	484	NE2	GLN	58	29.482	26.536	5.907	1.00	40.77
ATOM	485	C	GLN	58	27.495	26.449	2.866	1.00	25.89
ATOM	486	O	GLN	58	27.725	25.506	3.619	1.00	25.53
ATOM	487	N	ILE	59	26.264	26.794	2.511	1.00	24.98
ATOM	488	CA	ILE	59	25.104	26.049	2.985	1.00	22.92
ATOM	489	CB	ILE	59	23.787	26.717	2.531	1.00	23.63
ATOM	490	CG2	ILE	59	22.617	25.752	2.715	1.00	21.17
ATOM	491	CG1	ILE	59	23.570	28.021	3.307	1.00	22.62
ATOM	492	CD1	ILE	59	22.311	28.781	2.879	1.00	23.75
ATOM	493	C	ILE	59	25.133	24.618	2.448	1.00	23.06
ATOM	494	O	ILE	59	24.867	23.668	3.181	1.00	21.94
ATOM	495	N	THR	60	25.445	24.470	1.163	1.00	23.15
ATOM	496	CA	THR	60	25.510	23.149	0.552	1.00	23.53
ATOM	497	CB	THR	60	25.837	23.243	-0.956	1.00	22.65
ATOM	498	OG1	THR	60	24.787	23.946	-1.631	1.00	24.06
ATOM	499	CG2	THR	60	25.986	21.854	-1.562	1.00	22.93
ATOM	500	C	THR	60	26.596	22.333	1.244	1.00	22.48
ATOM	501	O	THR	60	26.423	21.148	1.514	1.00	24.18
ATOM	502	N	HIS	61	27.715	22.984	1.537	1.00	23.04
ATOM	503	CA	HIS	61	28.837	22.324	2.194	1.00	22.43
ATOM	504	CB	HIS	61	29.958	23.346	2.401	1.00	23.21
ATOM	505	CG	HIS	61	31.257	22.753	2.846	1.00	26.52
ATOM	506	CD2	HIS	61	32.298	23.298	3.520	1.00	28.76
ATOM	507	ND1	HIS	61	31.623	21.455	2.566	1.00	28.62
ATOM	508	CE1	HIS	61	32.830	21.224	3.049	1.00	27.83
ATOM	509	NE2	HIS	61	33.263	22.326	3.634	1.00	29.16
ATOM	510	C	HIS	61	28.356	21.753	3.528	1.00	22.71
ATOM	511	O	HIS	61	28.583	20.582	3.837	1.00	22.54
ATOM	512	N	ALA	62	27.659	22.579	4.297	1.00	21.43
ATOM	513	CA	ALA	62	27.141	22.168	5.596	1.00	22.12
ATOM	514	CB	ALA	62	26.597	23.392	6.349	1.00	17.66
ATOM	515	C	ALA	62	26.059	21.088	5.480	1.00	21.21
ATOM	516	O	ALA	62	25.959	20.208	6.340	1.00	22.10

ATOM	517	N	ILE	63	25.247	21.157	4.428	1.00	21.36
ATOM	518	CA	ILE	63	24.185	20.172	4.221	1.00	21.14
ATOM	519	CB	ILE	63	23.239	20.582	3.075	1.00	20.43
ATOM	520	CG2	ILE	63	22.333	19.429	2.711	1.00	20.13
ATOM	521	CG1	ILE	63	22.402	21.795	3.493	1.00	20.25
ATOM	522	CD1	ILE	63	21.416	22.260	2.425	1.00	22.13
ATOM	523	C	ILE	63	24.773	18.804	3.901	1.00	22.25
ATOM	524	O	ILE	63	24.238	17.779	4.323	1.00	22.39
ATOM	525	N	GLN	64	25.875	18.787	3.155	1.00	22.82
ATOM	526	CA	GLN	64	26.517	17.528	2.801	1.00	22.75
ATOM	527	CB	GLN	64	27.700	17.782	1.846	1.00	21.87
ATOM	528	CG	GLN	64	27.200	18.212	0.465	1.00	24.19
ATOM	529	CD	GLN	64	28.293	18.402	-0.582	1.00	26.74
ATOM	530	OE1	GLN	64	28.005	18.432	-1.783	1.00	29.29
ATOM	531	NE2	GLN	64	29.536	18.541	-0.140	1.00	22.66
ATOM	532	C	GLN	64	26.950	16.798	4.064	1.00	22.10
ATOM	533	O	GLN	64	26.872	15.575	4.139	1.00	21.93
ATOM	534	N	TYR	65	27.385	17.554	5.064	1.00	22.47
ATOM	535	CA	TYR	65	27.791	16.964	6.335	1.00	23.86
ATOM	536	CB	TYR	65	28.572	17.980	7.171	1.00	26.62
ATOM	537	CG	TYR	65	30.050	18.030	6.823	1.00	30.04
ATOM	538	CD1	TYR	65	30.895	16.963	7.140	1.00	32.17
ATOM	539	CE1	TYR	65	32.252	16.986	6.807	1.00	33.14
ATOM	540	CD2	TYR	65	30.599	19.128	6.160	1.00	30.53
ATOM	541	CE2	TYR	65	31.957	19.161	5.818	1.00	33.67
ATOM	542	CZ	TYR	65	32.777	18.086	6.147	1.00	36.28
ATOM	543	OH	TYR	65	34.122	18.109	5.821	1.00	40.50
ATOM	544	C	TYR	65	26.581	16.449	7.120	1.00	22.30
ATOM	545	O	TYR	65	26.702	15.498	7.888	1.00	23.33
ATOM	546	N	VAL	66	25.417	17.071	6.938	1.00	20.36
ATOM	547	CA	VAL	66	24.222	16.598	7.637	1.00	20.83
ATOM	548	CB	VAL	66	23.020	17.574	7.502	1.00	18.86
ATOM	549	CG1	VAL	66	21.784	16.965	8.176	1.00	19.22
ATOM	550	CG2	VAL	66	23.348	18.914	8.159	1.00	16.99
ATOM	551	C	VAL	66	23.830	15.246	7.040	1.00	20.81
ATOM	552	O	VAL	66	23.338	14.370	7.740	1.00	22.04
ATOM	553	N	VAL	67	24.048	15.085	5.739	1.00	22.31
ATOM	554	CA	VAL	67	23.740	13.830	5.062	1.00	21.44
ATOM	555	CB	VAL	67	23.989	13.943	3.544	1.00	22.66
ATOM	556	CG1	VAL	67	23.770	12.593	2.872	1.00	22.40
ATOM	557	CG2	VAL	67	23.047	14.992	2.939	1.00	23.72
ATOM	558	C	VAL	67	24.624	12.726	5.653	1.00	22.20
ATOM	559	O	VAL	67	24.160	11.616	5.913	1.00	22.69
ATOM	560	N	GLU	68	25.896	13.040	5.879	1.00	23.93
ATOM	561	CA	GLU	68	26.825	12.072	6.463	1.00	25.73
ATOM	562	CB	GLU	68	28.241	12.652	6.483	1.00	31.22
ATOM	563	CG	GLU	68	28.790	12.972	5.097	1.00	35.81
ATOM	564	CD	GLU	68	29.333	11.745	4.375	1.00	42.48
ATOM	565	OE1	GLU	68	28.652	10.692	4.362	1.00	42.24
ATOM	566	OE2	GLU	68	30.449	11.841	3.808	1.00	45.88
ATOM	567	C	GLU	68	26.366	11.749	7.882	1.00	25.40
ATOM	568	O	GLU	68	26.432	10.597	8.322	1.00	23.68
ATOM	569	N	PHE	69	25.896	12.776	8.590	1.00	23.61
ATOM	570	CA	PHE	69	25.386	12.633	9.956	1.00	22.83
ATOM	571	CB	PHE	69	24.885	14.001	10.448	1.00	21.69
ATOM	572	CG	PHE	69	24.252	13.989	11.822	1.00	24.10
ATOM	573	CD1	PHE	69	24.903	13.412	12.912	1.00	21.29
ATOM	574	CD2	PHE	69	23.018	14.613	12.034	1.00	23.32
ATOM	575	CE1	PHE	69	24.341	13.459	14.184	1.00	22.08
ATOM	576	CE2	PHE	69	22.444	14.667	13.308	1.00	20.43
ATOM	577	CZ	PHE	69	23.106	14.089	14.386	1.00	22.91
ATOM	578	C	PHE	69	24.253	11.598	9.967	1.00	23.85
ATOM	579	O	PHE	69	24.265	10.659	10.764	1.00	25.22
ATOM	580	N	ALA	70	23.292	11.757	9.058	1.00	23.28
ATOM	581	CA	ALA	70	22.151	10.851	8.962	1.00	22.31
ATOM	582	CB	ALA	70	21.163	11.382	7.926	1.00	22.02
ATOM	583	C	ALA	70	22.538	9.406	8.618	1.00	22.95
ATOM	584	O	ALA	70	22.011	8.457	9.205	1.00	21.88
ATOM	585	N	LYS	71	23.449	9.241	7.664	1.00	23.24
ATOM	586	CA	LYS	71	23.889	7.911	7.249	1.00	26.69
ATOM	587	CB	LYS	71	24.853	8.026	6.065	1.00	27.02
ATOM	588	CG	LYS	71	24.246	8.701	4.848	1.00	28.09
ATOM	589	CD	LYS	71	25.300	9.022	3.802	1.00	29.71
ATOM	590	CE	LYS	71	25.970	7.770	3.257	1.00	30.06
ATOM	591	NZ	LYS	71	26.968	8.147	2.221	1.00	33.92
ATOM	592	C	LYS	71	24.557	7.114	8.379	1.00	26.63
ATOM	593	O	LYS	71	24.536	5.880	8.370	1.00	26.95
ATOM	594	N	ARG	72	25.144	7.808	9.347	1.00	24.99
ATOM	595	CA	ARG	72	25.804	7.120	10.449	1.00	27.31
ATOM	596	CB	ARG	72	27.051	7.892	10.880	1.00	28.59
ATOM	597	CG	ARG	72	28.031	8.064	9.732	1.00	29.69

ATOM	598	CD	ARG	72	29.365	8.593	10.180	1.00	31.03
ATOM	599	NE	ARG	72	30.268	8.732	9.044	1.00	33.59
ATOM	600	CZ	ARG	72	31.546	9.081	9.145	1.00	38.36
ATOM	601	NH1	ARG	72	32.076	9.326	10.338	1.00	39.73
ATOM	602	NH2	ARG	72	32.291	9.194	8.054	1.00	39.15
ATOM	603	C	ARG	72	24.891	6.874	11.643	1.00	27.40
ATOM	604	O	ARG	72	25.333	6.367	12.675	1.00	29.05
ATOM	605	N	ILE	73	23.618	7.243	11.504	1.00	26.22
ATOM	606	CA	ILE	73	22.648	7.015	12.566	1.00	24.04
ATOM	607	CB	ILE	73	21.631	8.178	12.705	1.00	22.57
ATOM	608	CG2	ILE	73	20.568	7.810	13.744	1.00	23.16
ATOM	609	CG1	ILE	73	22.352	9.463	13.124	1.00	23.44
ATOM	610	CD1	ILE	73	21.412	10.645	13.411	1.00	23.02
ATOM	611	C	ILE	73	21.884	5.747	12.205	1.00	25.40
ATOM	612	O	ILE	73	21.067	5.737	11.276	1.00	23.63
ATOM	613	N	THR	74	22.155	4.679	12.947	1.00	25.29
ATOM	614	CA	THR	74	21.521	3.388	12.712	1.00	27.03
ATOM	615	CB	THR	74	21.790	2.433	13.878	1.00	29.63
ATOM	616	OG1	THR	74	23.157	2.555	14.286	1.00	33.21
ATOM	617	CG2	THR	74	21.531	0.998	13.445	1.00	33.49
ATOM	618	C	THR	74	20.007	3.466	12.510	1.00	25.59
ATOM	619	O	THR	74	19.479	2.985	11.508	1.00	25.68
ATOM	620	N	GLY	75	19.315	4.063	13.472	1.00	26.41
ATOM	621	CA	GLY	75	17.868	4.181	13.388	1.00	25.95
ATOM	622	C	GLY	75	17.382	4.896	12.139	1.00	25.86
ATOM	623	O	GLY	75	16.324	4.563	11.603	1.00	25.03
ATOM	624	N	PHE	76	18.146	5.877	11.667	1.00	24.84
ATOM	625	CA	PHE	76	17.752	6.612	10.466	1.00	25.41
ATOM	626	CB	PHE	76	18.643	7.847	10.259	1.00	23.08
ATOM	627	CG	PHE	76	18.319	8.634	9.005	1.00	25.15
ATOM	628	CD1	PHE	76	18.889	8.291	7.778	1.00	25.38
ATOM	629	CD2	PHE	76	17.443	9.714	9.050	1.00	23.74
ATOM	630	CE1	PHE	76	18.592	9.015	6.621	1.00	25.08
ATOM	631	CE2	PHE	76	17.140	10.445	7.891	1.00	24.62
ATOM	632	CZ	PHE	76	17.717	10.092	6.680	1.00	22.76
ATOM	633	C	PHE	76	17.828	5.717	9.240	1.00	24.88
ATOM	634	O	PHE	76	16.888	5.665	8.447	1.00	24.05
ATOM	635	N	MET	77	18.943	5.007	9.088	1.00	25.71
ATOM	636	CA	MET	77	19.123	4.136	7.937	1.00	26.70
ATOM	637	CB	MET	77	20.575	3.655	7.852	1.00	28.75
ATOM	638	CG	MET	77	21.577	4.773	7.554	1.00	30.31
ATOM	639	SD	MET	77	21.118	5.827	6.136	1.00	31.94
ATOM	640	CE	MET	77	21.818	4.891	4.717	1.00	35.36
ATOM	641	C	MET	77	18.164	2.947	7.920	1.00	28.58
ATOM	642	O	MET	77	18.071	2.233	6.919	1.00	28.47
ATOM	643	N	GLU	78	17.449	2.737	9.022	1.00	29.72
ATOM	644	CA	GLU	78	16.477	1.652	9.091	1.00	30.71
ATOM	645	CB	GLU	78	16.312	1.153	10.525	1.00	32.46
ATOM	646	CG	GLU	78	17.393	0.187	10.966	1.00	38.31
ATOM	647	CD	GLU	78	17.235	-0.231	12.411	1.00	40.71
ATOM	648	OE1	GLU	78	16.118	-0.633	12.794	1.00	43.62
ATOM	649	OE2	GLU	78	18.226	-0.160	13.163	1.00	43.48
ATOM	650	C	GLU	78	15.129	2.121	8.558	1.00	31.42
ATOM	651	O	GLU	78	14.226	1.315	8.336	1.00	29.99
ATOM	652	N	LEU	79	14.984	3.428	8.368	1.00	30.08
ATOM	653	CA	LEU	79	13.735	3.958	7.832	1.00	29.88
ATOM	654	CB	LEU	79	13.658	5.476	8.044	1.00	25.44
ATOM	655	CG	LEU	79	13.653	5.967	9.495	1.00	25.48
ATOM	656	CD1	LEU	79	13.735	7.483	9.516	1.00	23.35
ATOM	657	CD2	LEU	79	12.392	5.480	10.219	1.00	24.40
ATOM	658	C	LEU	79	13.745	3.633	6.339	1.00	29.03
ATOM	659	O	LEU	79	14.815	3.562	5.735	1.00	26.93
ATOM	660	N	CYS	80	12.573	3.419	5.744	1.00	30.41
ATOM	661	CA	CYS	80	12.524	3.114	4.314	1.00	32.22
ATOM	662	CB	CYS	80	11.081	2.931	3.830	1.00	33.77
ATOM	663	SG	CYS	80	10.113	4.443	3.665	1.00	35.11
ATOM	664	C	CYS	80	13.182	4.281	3.582	1.00	32.79
ATOM	665	O	CYS	80	13.107	5.432	4.032	1.00	31.43
ATOM	666	N	GLN	81	13.825	3.986	2.458	1.00	32.81
ATOM	667	CA	GLN	81	14.533	5.009	1.694	1.00	33.38
ATOM	668	CB	GLN	81	15.144	4.401	0.433	1.00	36.20
ATOM	669	CG	GLN	81	15.988	5.382	-0.353	1.00	40.19
ATOM	670	CD	GLN	81	16.894	4.693	-1.346	1.00	42.67
ATOM	671	OE1	GLN	81	16.429	4.055	-2.295	1.00	44.22
ATOM	672	NE2	GLN	81	18.201	4.808	-1.128	1.00	42.74
ATOM	673	C	GLN	81	13.702	6.225	1.317	1.00	32.60
ATOM	674	O	GLN	81	14.218	7.346	1.286	1.00	31.70
ATOM	675	N	ASN	82	12.423	6.017	1.019	1.00	30.05
ATOM	676	CA	ASN	82	11.571	7.139	0.655	1.00	29.42
ATOM	677	CB	ASN	82	10.160	6.665	0.317	1.00	30.85
ATOM	678	CG	ASN	82	9.211	7.818	0.086	1.00	33.27

ATOM	679	OD1	ASN	82	8.605	8.345	1.026	1.00	35.99
ATOM	680	ND2	ASN	82	9.091	8.236	-1.168	1.00	34.74
ATOM	681	C	ASN	82	11.508	8.175	1.775	1.00	27.40
ATOM	682	O	ASN	82	11.635	9.372	1.527	1.00	26.11
ATOM	683	N	ASP	83	11.310	7.716	3.008	1.00	26.77
ATOM	684	CA	ASP	83	11.236	8.635	4.140	1.00	25.04
ATOM	685	CB	ASP	83	10.629	7.921	5.354	1.00	24.28
ATOM	686	CG	ASP	83	9.136	7.649	5.175	1.00	25.67
ATOM	687	OD1	ASP	83	8.564	8.116	4.166	1.00	26.27
ATOM	688	OD2	ASP	83	8.531	6.978	6.034	1.00	25.59
ATOM	689	C	ASP	83	12.594	9.253	4.471	1.00	23.54
ATOM	690	O	ASP	83	12.663	10.407	4.886	1.00	24.66
ATOM	691	N	GLN	84	13.672	8.497	4.276	1.00	22.13
ATOM	692	CA	GLN	84	15.008	9.029	4.518	1.00	23.18
ATOM	693	CB	GLN	84	16.076	8.012	4.118	1.00	22.97
ATOM	694	CG	GLN	84	16.201	6.783	5.019	1.00	24.40
ATOM	695	CD	GLN	84	17.276	5.826	4.511	1.00	23.49
ATOM	696	OE1	GLN	84	18.170	6.233	3.777	1.00	24.96
ATOM	697	NE2	GLN	84	17.202	4.563	4.916	1.00	22.35
ATOM	698	C	GLN	84	15.176	10.290	3.663	1.00	24.86
ATOM	699	O	GLN	84	15.624	11.331	4.147	1.00	24.41
ATOM	700	N	ILE	85	14.819	10.175	2.384	1.00	24.70
ATOM	701	CA	ILE	85	14.908	11.283	1.433	1.00	24.80
ATOM	702	CB	ILE	85	14.426	10.838	0.013	1.00	26.48
ATOM	703	CG2	ILE	85	14.299	12.043	-0.917	1.00	23.15
ATOM	704	CG1	ILE	85	15.410	9.827	-0.588	1.00	26.97
ATOM	705	CD1	ILE	85	16.768	10.394	-0.861	1.00	29.45
ATOM	706	C	ILE	85	14.067	12.473	1.905	1.00	24.78
ATOM	707	O	ILE	85	14.539	13.614	1.914	1.00	25.40
ATOM	708	N	LEU	86	12.829	12.203	2.310	1.00	23.18
ATOM	709	CA	LEU	86	11.935	13.259	2.784	1.00	22.88
ATOM	710	CB	LEU	86	10.554	12.687	3.114	1.00	22.96
ATOM	711	CG	LEU	86	9.712	12.313	1.902	1.00	28.74
ATOM	712	CD1	LEU	86	8.410	11.644	2.366	1.00	27.61
ATOM	713	CD2	LEU	86	9.425	13.575	1.084	1.00	29.85
ATOM	714	C	LEU	86	12.480	13.973	4.013	1.00	21.25
ATOM	715	O	LEU	86	12.448	15.193	4.089	1.00	21.77
ATOM	716	N	LEU	87	12.965	13.213	4.986	1.00	22.23
ATOM	717	CA	LEU	87	13.510	13.821	6.196	1.00	20.76
ATOM	718	CB	LEU	87	13.946	12.736	7.186	1.00	20.64
ATOM	719	CG	LEU	87	12.830	11.876	7.789	1.00	20.81
ATOM	720	CD1	LEU	87	13.425	10.787	8.681	1.00	21.55
ATOM	721	CD2	LEU	87	11.901	12.762	8.590	1.00	21.01
ATOM	722	C	LEU	87	14.696	14.727	5.860	1.00	21.15
ATOM	723	O	LEU	87	14.808	15.842	6.367	1.00	21.87
ATOM	724	N	LEU	88	15.585	14.246	5.003	1.00	20.92
ATOM	725	CA	LEU	88	16.744	15.039	4.624	1.00	22.07
ATOM	726	CB	LEU	88	17.730	14.172	3.837	1.00	20.79
ATOM	727	CG	LEU	88	18.572	13.279	4.759	1.00	24.02
ATOM	728	CD1	LEU	88	19.333	12.241	3.956	1.00	21.15
ATOM	729	CD2	LEU	88	19.534	14.159	5.556	1.00	20.95
ATOM	730	C	LEU	88	16.380	16.293	3.831	1.00	22.47
ATOM	731	O	LEU	88	16.876	17.380	4.121	1.00	22.21
ATOM	732	N	LYS	89	15.505	16.153	2.841	1.00	24.00
ATOM	733	CA	LYS	89	15.106	17.303	2.028	1.00	25.58
ATOM	734	CB	LYS	89	14.174	16.855	0.897	1.00	28.38
ATOM	735	CG	LYS	89	13.626	18.006	0.053	1.00	33.25
ATOM	736	CD	LYS	89	12.677	17.499	-1.032	1.00	36.96
ATOM	737	CE	LYS	89	12.083	18.647	-1.857	1.00	40.68
ATOM	738	NZ	LYS	89	13.067	19.285	-2.776	1.00	41.21
ATOM	739	C	LYS	89	14.416	18.384	2.861	1.00	23.76
ATOM	740	O	LYS	89	14.693	19.572	2.716	1.00	23.44
ATOM	741	N	SER	90	13.518	17.972	3.745	1.00	24.58
ATOM	742	CA	SER	90	12.806	18.943	4.559	1.00	24.92
ATOM	743	CB	SER	90	11.462	18.359	5.011	1.00	25.41
ATOM	744	OG	SER	90	11.643	17.177	5.770	1.00	25.27
ATOM	745	C	SER	90	13.585	19.418	5.785	1.00	24.40
ATOM	746	O	SER	90	13.377	20.536	6.255	1.00	24.10
ATOM	747	N	GLY	91	14.493	18.587	6.290	1.00	22.98
ATOM	748	CA	GLY	91	15.210	18.966	7.496	1.00	22.61
ATOM	749	C	GLY	91	16.696	19.258	7.446	1.00	23.29
ATOM	750	O	GLY	91	17.268	19.627	8.473	1.00	22.29
ATOM	751	N	CYS	92	17.332	19.116	6.284	1.00	23.33
ATOM	752	CA	CYS	92	18.770	19.368	6.205	1.00	23.73
ATOM	753	CB	CYS	92	19.291	19.140	4.781	1.00	26.18
ATOM	754	SG	CYS	92	18.549	20.198	3.516	1.00	35.39
ATOM	755	C	CYS	92	19.151	20.772	6.668	1.00	22.55
ATOM	756	O	CYS	92	20.073	20.938	7.467	1.00	20.78
ATOM	757	N	LEU	93	18.442	21.782	6.176	1.00	20.74
ATOM	758	CA	LEU	93	18.762	23.153	6.549	1.00	20.88
ATOM	759	CB	LEU	93	18.001	24.147	5.659	1.00	19.11

ATOM	760	CG	LEU	93	18.457	25.615	5.791	1.00	22.77
ATOM	761	CD1	LEU	93	19.968	25.732	5.556	1.00	20.31
ATOM	762	CD2	LEU	93	17.689	26.483	4.787	1.00	21.80
ATOM	763	C	LEU	93	18.478	23.427	8.024	1.00	20.09
ATOM	764	O	LEU	93	19.190	24.205	8.667	1.00	21.56
ATOM	765	N	GLU	94	17.452	22.788	8.568	1.00	18.63
ATOM	766	CA	GLU	94	17.125	22.979	9.975	1.00	22.09
ATOM	767	CB	GLU	94	15.813	22.273	10.335	1.00	20.52
ATOM	768	CG	GLU	94	14.643	22.753	9.497	1.00	23.52
ATOM	769	CD	GLU	94	13.303	22.276	10.027	1.00	24.62
ATOM	770	OE1	GLU	94	13.285	21.458	10.972	1.00	25.58
ATOM	771	OE2	GLU	94	12.268	22.724	9.492	1.00	26.18
ATOM	772	C	GLU	94	18.267	22.440	10.828	1.00	21.56
ATOM	773	O	GLU	94	18.622	23.035	11.840	1.00	23.14
ATOM	774	N	VAL	95	18.847	21.315	10.419	1.00	22.47
ATOM	775	CA	VAL	95	19.970	20.757	11.167	1.00	21.92
ATOM	776	CB	VAL	95	20.358	19.348	10.660	1.00	20.19
ATOM	777	CG1	VAL	95	21.640	18.884	11.347	1.00	17.76
ATOM	778	CG2	VAL	95	19.230	18.359	10.954	1.00	21.38
ATOM	779	C	VAL	95	21.179	21.690	11.043	1.00	20.91
ATOM	780	O	VAL	95	21.891	21.921	12.022	1.00	23.34
ATOM	781	N	VAL	96	21.419	22.219	9.843	1.00	20.72
ATOM	782	CA	VAL	96	22.544	23.142	9.640	1.00	20.86
ATOM	783	CB	VAL	96	22.632	23.609	8.168	1.00	20.89
ATOM	784	CG1	VAL	96	23.622	24.766	8.034	1.00	21.60
ATOM	785	CG2	VAL	96	23.078	22.435	7.285	1.00	22.01
ATOM	786	C	VAL	96	22.384	24.369	10.545	1.00	20.92
ATOM	787	O	VAL	96	23.356	24.873	11.119	1.00	20.53
ATOM	788	N	LEU	97	21.151	24.847	10.672	1.00	21.56
ATOM	789	CA	LEU	97	20.879	26.008	11.507	1.00	22.41
ATOM	790	CB	LEU	97	19.414	26.427	11.382	1.00	24.63
ATOM	791	CG	LEU	97	19.039	27.746	12.062	1.00	27.57
ATOM	792	CD1	LEU	97	19.785	28.888	11.375	1.00	27.68
ATOM	793	CD2	LEU	97	17.522	27.969	11.984	1.00	27.40
ATOM	794	C	LEU	97	21.196	25.687	12.963	1.00	23.37
ATOM	795	O	LEU	97	21.774	26.510	13.670	1.00	24.02
ATOM	796	N	VAL	98	20.795	24.505	13.424	1.00	22.24
ATOM	797	CA	VAL	98	21.083	24.124	14.801	1.00	22.66
ATOM	798	CB	VAL	98	20.454	22.753	15.168	1.00	24.14
ATOM	799	CG1	VAL	98	20.950	22.295	16.540	1.00	21.61
ATOM	800	CG2	VAL	98	18.936	22.872	15.184	1.00	22.31
ATOM	801	C	VAL	98	22.598	24.041	14.977	1.00	21.26
ATOM	802	O	VAL	98	23.147	24.583	15.930	1.00	23.35
ATOM	803	N	ARG	99	23.275	23.381	14.043	1.00	21.04
ATOM	804	CA	ARG	99	24.728	23.238	14.126	1.00	22.66
ATOM	805	CB	ARG	99	25.241	22.338	12.997	1.00	21.34
ATOM	806	CG	ARG	99	24.958	20.860	13.204	1.00	19.68
ATOM	807	CD	ARG	99	25.493	20.040	12.042	1.00	20.91
ATOM	808	NE	ARG	99	25.596	18.628	12.392	1.00	19.97
ATOM	809	CZ	ARG	99	26.207	17.710	11.651	1.00	21.46
ATOM	810	NH1	ARG	99	26.774	18.047	10.499	1.00	19.48
ATOM	811	NH2	ARG	99	26.268	16.456	12.077	1.00	19.49
ATOM	812	C	ARG	99	25.444	24.586	14.068	1.00	23.66
ATOM	813	O	ARG	99	26.496	24.770	14.680	1.00	22.32
ATOM	814	N	MET	100	24.873	25.524	13.325	1.00	24.98
ATOM	815	CA	MET	100	25.468	26.849	13.200	1.00	26.11
ATOM	816	CB	MET	100	24.580	27.732	12.315	1.00	24.69
ATOM	817	CG	MET	100	25.125	29.131	12.096	1.00	28.62
ATOM	818	SD	MET	100	23.935	30.203	11.266	1.00	30.73
ATOM	819	CE	MET	100	22.917	30.695	12.620	1.00	28.23
ATOM	820	C	MET	100	25.647	27.500	14.580	1.00	26.32
ATOM	821	O	MET	100	26.560	28.303	14.791	1.00	25.50
ATOM	822	N	CYS	101	24.782	27.140	15.524	1.00	26.14
ATOM	823	CA	CYS	101	24.857	27.716	16.861	1.00	26.26
ATOM	824	CB	CYS	101	23.647	27.273	17.686	1.00	26.15
ATOM	825	SG	CYS	101	22.070	27.833	16.958	1.00	28.21
ATOM	826	C	CYS	101	26.155	27.369	17.579	1.00	26.31
ATOM	827	O	CYS	101	26.556	28.064	18.512	1.00	27.18
ATOM	828	N	ARG	102	26.810	26.300	17.134	1.00	26.05
ATOM	829	CA	ARG	102	28.080	25.863	17.715	1.00	25.81
ATOM	830	CB	ARG	102	28.487	24.477	17.194	1.00	24.97
ATOM	831	CG	ARG	102	27.477	23.360	17.374	1.00	24.25
ATOM	832	CD	ARG	102	27.899	22.131	16.567	1.00	24.77
ATOM	833	NE	ARG	102	29.120	21.499	17.075	1.00	24.27
ATOM	834	CZ	ARG	102	30.251	21.376	16.384	1.00	25.69
ATOM	835	NH1	ARG	102	30.334	21.847	15.146	1.00	22.95
ATOM	836	NH2	ARG	102	31.300	20.763	16.924	1.00	24.83
ATOM	837	C	ARG	102	29.167	26.837	17.290	1.00	25.16
ATOM	838	O	ARG	102	30.189	26.965	17.956	1.00	26.46
ATOM	839	N	ALA	103	28.949	27.499	16.158	1.00	25.50
ATOM	840	CA	ALA	103	29.925	28.438	15.610	1.00	24.73

ATOM	841	CB	ALA	103	30.282	28.031	14.191	1.00	24.76
ATOM	842	C	ALA	103	29.412	29.869	15.626	1.00	25.49
ATOM	843	O	ALA	103	29.663	30.641	14.696	1.00	26.25
ATOM	844	N	PHE	104	28.701	30.220	16.693	1.00	24.81
ATOM	845	CA	PHE	104	28.138	31.552	16.837	1.00	24.87
ATOM	846	CB	PHE	104	26.612	31.463	16.834	1.00	24.62
ATOM	847	CG	PHE	104	25.912	32.800	16.868	1.00	27.48
ATOM	848	CD1	PHE	104	25.548	33.383	18.082	1.00	27.30
ATOM	849	CD2	PHE	104	25.599	33.465	15.685	1.00	25.70
ATOM	850	CE1	PHE	104	24.876	34.610	18.115	1.00	27.97
ATOM	851	CE2	PHE	104	24.930	34.693	15.708	1.00	26.67
ATOM	852	CZ	PHE	104	24.568	35.263	16.923	1.00	25.05
ATOM	853	C	PHE	104	28.637	32.156	18.145	1.00	26.24
ATOM	854	O	PHE	104	28.624	31.504	19.188	1.00	25.16
ATOM	855	N	ASN	105	29.095	33.398	18.078	1.00	24.14
ATOM	856	CA	ASN	105	29.594	34.080	19.259	1.00	25.15
ATOM	857	CB	ASN	105	30.833	34.889	18.884	1.00	25.27
ATOM	858	CG	ASN	105	31.414	35.640	20.054	1.00	28.22
ATOM	859	OD1	ASN	105	30.811	35.715	21.125	1.00	29.75
ATOM	860	ND2	ASN	105	32.592	36.211	19.853	1.00	28.02
ATOM	861	C	ASN	105	28.471	34.999	19.744	1.00	25.46
ATOM	862	O	ASN	105	28.218	36.043	19.148	1.00	23.70
ATOM	863	N	PRO	106	27.704	34.615	20.835	1.00	26.30
ATOM	864	CD	PRO	106	27.965	33.373	21.611	1.00	27.28
ATOM	865	CA	PRO	106	26.680	35.414	21.382	1.00	27.94
ATOM	866	CB	PRO	106	25.995	34.442	22.339	1.00	27.49
ATOM	867	CG	PRO	106	27.150	33.646	22.867	1.00	27.98
ATOM	868	C	PRO	106	27.052	36.731	22.059	1.00	28.50
ATOM	869	O	PRO	106	26.169	37.481	22.470	1.00	29.76
ATOM	870	N	LEU	107	28.344	37.024	22.173	1.00	28.28
ATOM	871	CA	LEU	107	28.761	38.277	22.800	1.00	30.25
ATOM	872	CB	LEU	107	30.150	38.138	23.444	1.00	28.28
ATOM	873	CG	LEU	107	30.176	37.231	24.686	1.00	31.14
ATOM	874	CD1	LEU	107	31.562	37.188	25.277	1.00	29.40
ATOM	875	CD2	LEU	107	29.192	37.746	25.726	1.00	32.31
ATOM	876	C	LEU	107	28.758	39.433	21.807	1.00	29.75
ATOM	877	O	LEU	107	28.332	40.533	22.142	1.00	31.64
ATOM	878	N	ASN	108	29.231	39.193	20.589	1.00	28.78
ATOM	879	CA	ASN	108	29.249	40.246	19.580	1.00	28.18
ATOM	880	CB	ASN	108	30.681	40.517	19.107	1.00	27.56
ATOM	881	CG	ASN	108	31.362	39.279	18.538	1.00	28.12
ATOM	882	OD1	ASN	108	30.733	38.238	18.347	1.00	26.25
ATOM	883	ND2	ASN	108	32.657	39.396	18.257	1.00	24.43
ATOM	884	C	ASN	108	28.364	39.894	18.386	1.00	27.75
ATOM	885	O	ASN	108	28.432	40.537	17.343	1.00	27.33
ATOM	886	N	ASN	109	27.535	38.870	18.556	1.00	27.69
ATOM	887	CA	ASN	109	26.627	38.418	17.512	1.00	28.83
ATOM	888	CB	ASN	109	25.465	39.395	17.353	1.00	29.93
ATOM	889	CG	ASN	109	24.546	39.387	18.543	1.00	32.72
ATOM	890	OD1	ASN	109	24.216	38.324	19.072	1.00	32.17
ATOM	891	ND2	ASN	109	24.116	40.575	18.973	1.00	31.31
ATOM	892	C	ASN	109	27.293	38.222	16.164	1.00	27.63
ATOM	893	O	ASN	109	26.918	38.861	15.183	1.00	27.80
ATOM	894	N	THR	110	28.287	37.342	16.124	1.00	26.91
ATOM	895	CA	THR	110	28.990	37.042	14.889	1.00	26.50
ATOM	896	CB	THR	110	30.469	37.468	14.967	1.00	25.46
ATOM	897	OG1	THR	110	31.071	36.887	16.130	1.00	24.60
ATOM	898	CG2	THR	110	30.587	38.987	15.050	1.00	26.91
ATOM	899	C	THR	110	28.908	35.535	14.668	1.00	26.44
ATOM	900	O	THR	110	28.813	34.765	15.625	1.00	26.49
ATOM	901	N	VAL	111	28.928	35.124	13.407	1.00	25.62
ATOM	902	CA	VAL	111	28.859	33.713	13.058	1.00	25.05
ATOM	903	CB	VAL	111	27.550	33.386	12.292	1.00	26.15
ATOM	904	CG1	VAL	111	27.581	34.012	10.893	1.00	25.65
ATOM	905	CG2	VAL	111	27.364	31.875	12.207	1.00	25.76
ATOM	906	C	VAL	111	30.056	33.361	12.178	1.00	25.27
ATOM	907	O	VAL	111	30.541	34.204	11.415	1.00	24.98
ATOM	908	N	LEU	112	30.536	32.126	12.302	1.00	23.55
ATOM	909	CA	LEU	112	31.677	31.660	11.520	1.00	24.51
ATOM	910	CB	LEU	112	32.171	30.316	12.067	1.00	24.17
ATOM	911	CG	LEU	112	33.323	29.570	11.384	1.00	26.81
ATOM	912	CD1	LEU	112	34.579	30.439	11.321	1.00	24.50
ATOM	913	CD2	LEU	112	33.603	28.292	12.176	1.00	26.23
ATOM	914	C	LEU	112	31.251	31.512	10.063	1.00	25.07
ATOM	915	O	LEU	112	30.347	30.734	9.751	1.00	23.68
ATOM	916	N	PHE	113	31.905	32.267	9.183	1.00	25.79
ATOM	917	CA	PHE	113	31.595	32.240	7.759	1.00	27.26
ATOM	918	CB	PHE	113	30.686	33.415	7.399	1.00	26.26
ATOM	919	CG	PHE	113	30.216	33.399	5.975	1.00	26.51
ATOM	920	CD1	PHE	113	29.338	32.412	5.528	1.00	27.75
ATOM	921	CD2	PHE	113	30.661	34.358	5.073	1.00	26.90

ATOM	922	CE1	PHE	113	28.910	32.380	4.199	1.00	27.83
ATOM	923	CE2	PHE	113	30.239	34.336	3.736	1.00	27.68
ATOM	924	CZ	PHE	113	29.361	33.344	3.302	1.00	26.77
ATOM	925	C	PHE	113	32.885	32.318	6.954	1.00	28.10
ATOM	926	O	PHE	113	33.651	33.271	7.079	1.00	29.91
ATOM	927	N	GLU	114	33.117	31.310	6.122	1.00	30.65
ATOM	928	CA	GLU	114	34.325	31.243	5.312	1.00	31.06
ATOM	929	CB	GLU	114	34.296	32.295	4.188	1.00	30.36
ATOM	930	CG	GLU	114	33.108	32.146	3.220	1.00	33.61
ATOM	931	CD	GLU	114	33.194	33.074	2.006	1.00	36.26
ATOM	932	OE1	GLU	114	33.847	34.137	2.098	1.00	37.14
ATOM	933	OE2	GLU	114	32.596	32.746	0.960	1.00	36.76
ATOM	934	C	GLU	114	35.579	31.416	6.169	1.00	31.09
ATOM	935	O	GLU	114	36.425	32.267	5.893	1.00	29.44
ATOM	936	N	GLY	115	35.678	30.619	7.232	1.00	31.65
ATOM	937	CA	GLY	115	36.862	30.653	8.077	1.00	31.02
ATOM	938	C	GLY	115	36.987	31.636	9.227	1.00	31.03
ATOM	939	O	GLY	115	37.850	31.453	10.081	1.00	31.02
ATOM	940	N	LYS	116	36.165	32.678	9.266	1.00	30.47
ATOM	941	CA	LYS	116	36.247	33.640	10.364	1.00	29.13
ATOM	942	CB	LYS	116	37.081	34.850	9.950	1.00	31.65
ATOM	943	CG	LYS	116	38.518	34.542	9.546	1.00	35.17
ATOM	944	CD	LYS	116	39.156	35.784	8.933	1.00	39.50
ATOM	945	CE	LYS	116	40.598	35.550	8.517	1.00	41.93
ATOM	946	NZ	LYS	116	41.482	35.336	9.699	1.00	46.16
ATOM	947	C	LYS	116	34.855	34.108	10.773	1.00	28.58
ATOM	948	O	LYS	116	33.883	33.914	10.035	1.00	25.83
ATOM	949	N	TYR	117	34.773	34.731	11.947	1.00	26.38
ATOM	950	CA	TYR	117	33.513	35.241	12.473	1.00	26.28
ATOM	951	CB	TYR	117	33.557	35.311	14.006	1.00	27.82
ATOM	952	CG	TYR	117	33.470	33.964	14.684	1.00	25.87
ATOM	953	CD1	TYR	117	34.524	33.048	14.605	1.00	27.04
ATOM	954	CE1	TYR	117	34.426	31.782	15.190	1.00	26.50
ATOM	955	CD2	TYR	117	32.316	33.585	15.369	1.00	23.65
ATOM	956	CE2	TYR	117	32.208	32.329	15.953	1.00	26.33
ATOM	957	CZ	TYR	117	33.263	31.433	15.858	1.00	26.31
ATOM	958	OH	TYR	117	33.136	30.179	16.405	1.00	29.08
ATOM	959	C	TYR	117	33.191	36.624	11.922	1.00	27.89
ATOM	960	O	TYR	117	34.063	37.491	11.837	1.00	27.82
ATOM	961	N	GLY	118	31.932	36.821	11.551	1.00	27.62
ATOM	962	CA	GLY	118	31.503	38.104	11.029	1.00	27.35
ATOM	963	C	GLY	118	30.086	38.415	11.476	1.00	27.40
ATOM	964	O	GLY	118	29.275	37.502	11.644	1.00	26.12
ATOM	965	N	GLY	119	29.787	39.698	11.673	1.00	27.51
ATOM	966	CA	GLY	119	28.455	40.092	12.104	1.00	28.25
ATOM	967	C	GLY	119	27.465	39.994	10.964	1.00	30.48
ATOM	968	O	GLY	119	27.845	39.624	9.852	1.00	32.66
ATOM	969	N	MET	120	26.203	40.328	11.215	1.00	30.06
ATOM	970	CA	MET	120	25.200	40.245	10.159	1.00	33.29
ATOM	971	CB	MET	120	23.786	40.417	10.742	1.00	35.95
ATOM	972	CG	MET	120	23.464	41.793	11.321	1.00	40.01
ATOM	973	SD	MET	120	23.194	43.077	10.066	1.00	44.66
ATOM	974	CE	MET	120	21.580	42.608	9.449	1.00	38.51
ATOM	975	C	MET	120	25.423	41.233	9.010	1.00	33.96
ATOM	976	O	MET	120	24.889	41.036	7.916	1.00	32.84
ATOM	977	N	GLN	121	26.218	42.280	9.245	1.00	34.68
ATOM	978	CA	GLN	121	26.489	43.281	8.209	1.00	36.23
ATOM	979	CB	GLN	121	27.204	44.509	8.794	1.00	37.39
ATOM	980	CG	GLN	121	28.683	44.292	9.088	1.00	40.21
ATOM	981	CD	GLN	121	28.930	43.759	10.485	1.00	42.57
ATOM	982	OE1	GLN	121	28.035	43.184	11.111	1.00	42.30
ATOM	983	NE2	GLN	121	30.154	43.943	10.982	1.00	43.39
ATOM	984	C	GLN	121	27.357	42.670	7.117	1.00	36.52
ATOM	985	O	GLN	121	27.577	43.263	6.062	1.00	38.05
ATOM	986	N	MET	122	27.852	41.474	7.397	1.00	35.28
ATOM	987	CA	MET	122	28.686	40.731	6.474	1.00	32.99
ATOM	988	CB	MET	122	29.324	39.562	7.239	1.00	34.32
ATOM	989	CG	MET	122	30.068	38.536	6.417	1.00	32.66
ATOM	990	SD	MET	122	31.016	37.409	7.491	1.00	32.03
ATOM	991	CE	MET	122	29.704	36.572	8.406	1.00	29.49
ATOM	992	C	MET	122	27.819	40.225	5.317	1.00	33.06
ATOM	993	O	MET	122	28.315	39.986	4.219	1.00	31.80
ATOM	994	N	PHE	123	26.519	40.094	5.571	1.00	31.66
ATOM	995	CA	PHE	123	25.565	39.596	4.580	1.00	32.27
ATOM	996	CB	PHE	123	24.640	38.567	5.235	1.00	29.78
ATOM	997	CG	PHE	123	25.366	37.400	5.838	1.00	30.41
ATOM	998	CD1	PHE	123	25.875	36.387	5.030	1.00	28.95
ATOM	999	CD2	PHE	123	25.553	37.318	7.213	1.00	28.84
ATOM	1000	CE1	PHE	123	26.556	35.307	5.586	1.00	28.63
ATOM	1001	CE2	PHE	123	26.234	36.243	7.779	1.00	28.70
ATOM	1002	CZ	PHE	123	26.736	35.235	6.965	1.00	29.76

ATOM	1003	C	PHE	123	24.709	40.695	3.952	1.00	33.01
ATOM	1004	O	PHE	123	23.671	40.410	3.352	1.00	32.84
ATOM	1005	N	LYS	124	25.149	41.941	4.082	1.00	33.57
ATOM	1006	CA	LYS	124	24.409	43.075	3.542	1.00	35.39
ATOM	1007	CB	LYS	124	25.228	44.361	3.737	1.00	38.66
ATOM	1008	CG	LYS	124	24.439	45.645	3.501	1.00	43.12
ATOM	1009	CD	LYS	124	23.162	45.650	4.341	1.00	46.67
ATOM	1010	CE	LYS	124	22.286	46.866	4.040	1.00	49.30
ATOM	1011	NZ	LYS	124	20.975	46.787	4.753	1.00	48.16
ATOM	1012	C	LYS	124	24.005	42.923	2.071	1.00	33.97
ATOM	1013	O	LYS	124	22.858	43.169	1.719	1.00	34.76
ATOM	1014	N	ALA	125	24.936	42.497	1.219	1.00	34.80
ATOM	1015	CA	ALA	125	24.666	42.347	-0.215	1.00	34.52
ATOM	1016	CB	ALA	125	25.955	41.965	-0.953	1.00	33.38
ATOM	1017	C	ALA	125	23.548	41.366	-0.583	1.00	35.75
ATOM	1018	O	ALA	125	23.125	41.313	-1.738	1.00	35.49
ATOM	1019	N	LEU	126	23.071	40.581	0.378	1.00	35.88
ATOM	1020	CA	LEU	126	21.993	39.640	0.085	1.00	35.88
ATOM	1021	CB	LEU	126	21.877	38.583	1.181	1.00	34.67
ATOM	1022	CG	LEU	126	23.019	37.586	1.309	1.00	33.16
ATOM	1023	CD1	LEU	126	22.701	36.629	2.442	1.00	33.20
ATOM	1024	CD2	LEU	126	23.200	36.831	-0.006	1.00	31.66
ATOM	1025	C	LEU	126	20.661	40.360	-0.037	1.00	35.66
ATOM	1026	O	LEU	126	19.745	39.881	-0.699	1.00	37.30
ATOM	1027	N	GLY	127	20.556	41.509	0.618	1.00	36.88
ATOM	1028	CA	GLY	127	19.319	42.261	0.577	1.00	37.45
ATOM	1029	C	GLY	127	18.231	41.495	1.295	1.00	38.00
ATOM	1030	O	GLY	127	17.047	41.645	0.992	1.00	37.47
ATOM	1031	N	SER	128	18.637	40.672	2.257	1.00	38.76
ATOM	1032	CA	SER	128	17.696	39.862	3.024	1.00	38.85
ATOM	1033	CB	SER	128	17.783	38.399	2.575	1.00	39.65
ATOM	1034	OG	SER	128	17.675	38.280	1.167	1.00	40.93
ATOM	1035	C	SER	128	18.004	39.946	4.518	1.00	38.88
ATOM	1036	O	SER	128	18.142	38.916	5.184	1.00	38.92
ATOM	1037	N	ASP	129	18.104	41.160	5.050	1.00	38.31
ATOM	1038	CA	ASP	129	18.413	41.327	6.469	1.00	37.76
ATOM	1039	CB	ASP	129	18.513	42.809	6.837	1.00	38.81
ATOM	1040	CG	ASP	129	19.785	43.458	6.322	1.00	37.85
ATOM	1041	OD1	ASP	129	20.698	42.734	5.884	1.00	39.00
ATOM	1042	OD2	ASP	129	19.877	44.700	6.369	1.00	40.89
ATOM	1043	C	ASP	129	17.399	40.651	7.382	1.00	37.23
ATOM	1044	O	ASP	129	17.734	40.238	8.490	1.00	36.42
ATOM	1045	N	ASP	130	16.156	40.542	6.930	1.00	36.72
ATOM	1046	CA	ASP	130	15.143	39.901	7.755	1.00	36.80
ATOM	1047	CB	ASP	130	13.760	40.044	7.110	1.00	38.13
ATOM	1048	CG	ASP	130	13.722	39.535	5.688	1.00	40.50
ATOM	1049	OD1	ASP	130	14.726	39.717	4.969	1.00	40.76
ATOM	1050	OD2	ASP	130	12.680	38.969	5.285	1.00	41.30
ATOM	1051	C	ASP	130	15.507	38.430	7.958	1.00	34.04
ATOM	1052	O	ASP	130	15.376	37.899	9.058	1.00	32.59
ATOM	1053	N	LEU	131	15.974	37.779	6.897	1.00	31.60
ATOM	1054	CA	LEU	131	16.368	36.380	6.994	1.00	29.28
ATOM	1055	CB	LEU	131	16.735	35.812	5.615	1.00	28.37
ATOM	1056	CG	LEU	131	17.529	34.490	5.653	1.00	28.49
ATOM	1057	CD1	LEU	131	16.701	33.410	6.352	1.00	26.24
ATOM	1058	CD2	LEU	131	17.895	34.046	4.249	1.00	25.43
ATOM	1059	C	LEU	131	17.569	36.270	7.924	1.00	28.88
ATOM	1060	O	LEU	131	17.560	35.495	8.882	1.00	28.78
ATOM	1061	N	VAL	132	18.603	37.058	7.646	1.00	28.88
ATOM	1062	CA	VAL	132	19.805	37.032	8.473	1.00	28.97
ATOM	1063	CB	VAL	132	20.843	38.038	7.953	1.00	28.69
ATOM	1064	CG1	VAL	132	22.086	37.998	8.822	1.00	27.42
ATOM	1065	CG2	VAL	132	21.195	37.706	6.512	1.00	29.10
ATOM	1066	C	VAL	132	19.490	37.319	9.943	1.00	29.17
ATOM	1067	O	VAL	132	19.912	36.571	10.831	1.00	29.93
ATOM	1068	N	ASN	133	18.748	38.395	10.198	1.00	29.09
ATOM	1069	CA	ASN	133	18.367	38.759	11.562	1.00	28.91
ATOM	1070	CB	ASN	133	17.477	40.004	11.552	1.00	31.79
ATOM	1071	CG	ASN	133	18.275	41.297	11.466	1.00	35.19
ATOM	1072	OD1	ASN	133	17.728	42.352	11.149	1.00	36.03
ATOM	1073	ND2	ASN	133	19.569	41.222	11.765	1.00	34.40
ATOM	1074	C	ASN	133	17.634	37.620	12.266	1.00	28.71
ATOM	1075	O	ASN	133	17.850	37.376	13.453	1.00	28.36
ATOM	1076	N	GLU	134	16.758	36.928	11.546	1.00	27.60
ATOM	1077	CA	GLU	134	16.033	35.815	12.154	1.00	29.70
ATOM	1078	CB	GLU	134	14.904	35.340	11.235	1.00	30.25
ATOM	1079	CG	GLU	134	13.612	36.130	11.441	1.00	37.54
ATOM	1080	CD	GLU	134	12.429	35.572	10.672	1.00	39.03
ATOM	1081	OE1	GLU	134	12.311	34.333	10.568	1.00	42.45
ATOM	1082	OE2	GLU	134	11.604	36.376	10.186	1.00	43.40
ATOM	1083	C	GLU	134	16.978	34.659	12.484	1.00	28.63

ATOM	1084	O	GLU	134	16.867	34.040	13.540	1.00	27.53
ATOM	1085	N	ALA	135	17.916	34.385	11.583	1.00	28.23
ATOM	1086	CA	ALA	135	18.887	33.317	11.791	1.00	27.00
ATOM	1087	CB	ALA	135	19.769	33.178	10.571	1.00	26.34
ATOM	1088	C	ALA	135	19.734	33.636	13.019	1.00	27.05
ATOM	1089	O	ALA	135	19.955	32.774	13.876	1.00	25.93
ATOM	1090	N	PHE	136	20.199	34.881	13.104	1.00	27.53
ATOM	1091	CA	PHE	136	21.018	35.322	14.229	1.00	28.38
ATOM	1092	CB	PHE	136	21.569	36.728	13.963	1.00	29.04
ATOM	1093	CG	PHE	136	22.817	36.742	13.123	1.00	27.20
ATOM	1094	CD1	PHE	136	22.858	36.084	11.898	1.00	28.97
ATOM	1095	CD2	PHE	136	23.954	37.422	13.555	1.00	28.84
ATOM	1096	CE1	PHE	136	24.014	36.103	11.114	1.00	28.21
ATOM	1097	CE2	PHE	136	25.117	37.446	12.776	1.00	27.38
ATOM	1098	CZ	PHE	136	25.143	36.785	11.555	1.00	27.06
ATOM	1099	C	PHE	136	20.278	35.306	15.566	1.00	29.12
ATOM	1100	O	PHE	136	20.834	34.876	16.581	1.00	27.78
ATOM	1101	N	ASP	137	19.031	35.772	15.573	1.00	30.75
ATOM	1102	CA	ASP	137	18.247	35.798	16.808	1.00	31.48
ATOM	1103	CB	ASP	137	16.888	36.463	16.570	1.00	34.88
ATOM	1104	CG	ASP	137	17.013	37.938	16.197	1.00	39.69
ATOM	1105	OD1	ASP	137	18.118	38.513	16.338	1.00	41.72
ATOM	1106	OD2	ASP	137	15.997	38.524	15.769	1.00	41.77
ATOM	1107	C	ASP	137	18.046	34.388	17.361	1.00	30.07
ATOM	1108	O	ASP	137	18.094	34.173	18.572	1.00	28.12
ATOM	1109	N	PHE	138	17.814	33.430	16.470	1.00	29.22
ATOM	1110	CA	PHE	138	17.635	32.043	16.888	1.00	27.56
ATOM	1111	CB	PHE	138	17.284	31.156	15.692	1.00	26.66
ATOM	1112	CG	PHE	138	17.481	29.693	15.964	1.00	27.08
ATOM	1113	CD1	PHE	138	16.631	29.018	16.833	1.00	27.62
ATOM	1114	CD2	PHE	138	18.562	29.010	15.414	1.00	25.94
ATOM	1115	CE1	PHE	138	16.854	27.679	17.157	1.00	27.42
ATOM	1116	CE2	PHE	138	18.798	27.671	15.731	1.00	26.61
ATOM	1117	CZ	PHE	138	17.942	27.005	16.606	1.00	27.10
ATOM	1118	C	PHE	138	18.931	31.524	17.520	1.00	26.65
ATOM	1119	O	PHE	138	18.932	30.996	18.638	1.00	25.79
ATOM	1120	N	ALA	139	20.028	31.673	16.783	1.00	26.86
ATOM	1121	CA	ALA	139	21.335	31.228	17.246	1.00	28.26
ATOM	1122	CB	ALA	139	22.409	31.620	16.246	1.00	24.42
ATOM	1123	C	ALA	139	21.629	31.854	18.598	1.00	29.32
ATOM	1124	O	ALA	139	22.062	31.175	19.523	1.00	29.76
ATOM	1125	N	LYS	140	21.388	33.154	18.705	1.00	30.35
ATOM	1126	CA	LYS	140	21.628	33.857	19.955	1.00	33.43
ATOM	1127	CB	LYS	140	21.305	35.345	19.795	1.00	35.05
ATOM	1128	CG	LYS	140	21.512	36.156	21.056	1.00	41.64
ATOM	1129	CD	LYS	140	21.304	37.645	20.808	1.00	45.36
ATOM	1130	CE	LYS	140	21.412	38.426	22.113	1.00	48.64
ATOM	1131	NZ	LYS	140	22.648	38.062	22.869	1.00	48.83
ATOM	1132	C	LYS	140	20.784	33.250	21.072	1.00	32.60
ATOM	1133	O	LYS	140	21.271	33.018	22.173	1.00	33.54
ATOM	1134	N	ASN	141	19.520	32.968	20.782	1.00	33.89
ATOM	1135	CA	ASN	141	18.645	32.397	21.794	1.00	34.26
ATOM	1136	CB	ASN	141	17.187	32.488	21.351	1.00	35.65
ATOM	1137	CG	ASN	141	16.714	33.922	21.246	1.00	41.37
ATOM	1138	OD1	ASN	141	17.033	34.759	22.102	1.00	41.73
ATOM	1139	ND2	ASN	141	15.944	34.218	20.203	1.00	43.55
ATOM	1140	C	ASN	141	18.993	30.961	22.155	1.00	32.74
ATOM	1141	O	ASN	141	18.857	30.565	23.307	1.00	32.51
ATOM	1142	N	LEU	142	19.439	30.178	21.180	1.00	31.43
ATOM	1143	CA	LEU	142	19.800	28.800	21.475	1.00	29.57
ATOM	1144	CB	LEU	142	20.061	28.009	20.190	1.00	31.15
ATOM	1145	CG	LEU	142	20.302	26.512	20.415	1.00	30.62
ATOM	1146	CD1	LEU	142	19.000	25.852	20.835	1.00	28.71
ATOM	1147	CD2	LEU	142	20.824	25.870	19.149	1.00	30.61
ATOM	1148	C	LEU	142	21.058	28.809	22.329	1.00	28.67
ATOM	1149	O	LEU	142	21.188	28.022	23.266	1.00	27.68
ATOM	1150	N	CYS	143	21.988	29.706	22.004	1.00	28.64
ATOM	1151	CA	CYS	143	23.240	29.805	22.751	1.00	28.53
ATOM	1152	CB	CYS	143	24.164	30.857	22.118	1.00	29.40
ATOM	1153	SG	CYS	143	25.058	30.297	20.626	1.00	30.27
ATOM	1154	C	CYS	143	23.011	30.141	24.225	1.00	28.51
ATOM	1155	O	CYS	143	23.811	29.764	25.083	1.00	27.46
ATOM	1156	N	SER	144	21.922	30.844	24.524	1.00	27.47
ATOM	1157	CA	SER	144	21.631	31.204	25.907	1.00	30.41
ATOM	1158	CB	SER	144	20.407	32.123	25.978	1.00	30.97
ATOM	1159	OG	SER	144	19.221	31.404	25.687	1.00	32.16
ATOM	1160	C	SER	144	21.391	29.963	26.776	1.00	30.53
ATOM	1161	O	SER	144	21.527	30.024	27.995	1.00	31.62
ATOM	1162	N	LEU	145	21.039	28.841	26.147	1.00	29.38
ATOM	1163	CA	LEU	145	20.787	27.600	26.878	1.00	28.47
ATOM	1164	CB	LEU	145	19.886	26.664	26.062	1.00	30.06

ATOM	1165	CG	LEU	145	18.452	27.120	25.776	1.00	30.81
ATOM	1166	CD1	LEU	145	17.736	26.074	24.929	1.00	31.42
ATOM	1167	CD2	LEU	145	17.711	27.326	27.092	1.00	32.81
ATOM	1168	C	LEU	145	22.078	26.869	27.242	1.00	27.00
ATOM	1169	O	LEU	145	22.060	25.936	28.041	1.00	26.93
ATOM	1170	N	GLN	146	23.192	27.285	26.647	1.00	27.19
ATOM	1171	CA	GLN	146	24.481	26.669	26.938	1.00	28.35
ATOM	1172	CB	GLN	146	24.912	27.015	28.364	1.00	31.85
ATOM	1173	CG	GLN	146	25.051	28.488	28.638	1.00	37.93
ATOM	1174	CD	GLN	146	26.153	29.120	27.823	1.00	43.03
ATOM	1175	OE1	GLN	146	27.326	28.736	27.920	1.00	45.91
ATOM	1176	NE2	GLN	146	25.785	30.096	27.005	1.00	46.57
ATOM	1177	C	GLN	146	24.451	25.147	26.797	1.00	28.31
ATOM	1178	O	GLN	146	24.803	24.425	27.738	1.00	28.78
ATOM	1179	N	LEU	147	24.035	24.657	25.634	1.00	24.96
ATOM	1180	CA	LEU	147	23.971	23.219	25.405	1.00	25.05
ATOM	1181	CB	LEU	147	23.129	22.919	24.166	1.00	24.70
ATOM	1182	CG	LEU	147	21.682	23.401	24.168	1.00	25.61
ATOM	1183	CD1	LEU	147	21.020	22.977	22.858	1.00	27.01
ATOM	1184	CD2	LEU	147	20.945	22.817	25.369	1.00	26.03
ATOM	1185	C	LEU	147	25.357	22.616	25.206	1.00	25.19
ATOM	1186	O	LEU	147	26.253	23.262	24.664	1.00	25.02
ATOM	1187	N	THR	148	25.533	21.377	25.650	1.00	25.71
ATOM	1188	CA	THR	148	26.809	20.697	25.473	1.00	25.53
ATOM	1189	CB	THR	148	27.004	19.561	26.495	1.00	25.85
ATOM	1190	OG1	THR	148	25.986	18.572	26.297	1.00	25.37
ATOM	1191	CG2	THR	148	26.933	20.101	27.937	1.00	25.32
ATOM	1192	C	THR	148	26.777	20.078	24.076	1.00	26.33
ATOM	1193	O	THR	148	25.741	20.098	23.395	1.00	23.91
ATOM	1194	N	GLU	149	27.906	19.528	23.647	1.00	24.54
ATOM	1195	CA	GLU	149	27.973	18.898	22.335	1.00	25.20
ATOM	1196	CB	GLU	149	29.420	18.498	22.007	1.00	24.58
ATOM	1197	CG	GLU	149	30.257	19.657	21.475	1.00	27.87
ATOM	1198	CD	GLU	149	29.926	20.009	20.024	1.00	28.51
ATOM	1199	OE1	GLU	149	30.532	19.410	19.113	1.00	28.15
ATOM	1200	OE2	GLU	149	29.053	20.877	19.794	1.00	30.62
ATOM	1201	C	GLU	149	27.052	17.684	22.268	1.00	24.09
ATOM	1202	O	GLU	149	26.472	17.403	21.225	1.00	26.05
ATOM	1203	N	GLU	150	26.904	16.968	23.377	1.00	24.30
ATOM	1204	CA	GLU	150	26.034	15.789	23.393	1.00	24.51
ATOM	1205	CB	GLU	150	26.163	15.027	24.712	1.00	24.35
ATOM	1206	CG	GLU	150	27.526	14.403	24.987	1.00	28.10
ATOM	1207	CD	GLU	150	27.522	13.586	26.280	1.00	31.06
ATOM	1208	OE1	GLU	150	26.883	14.030	27.258	1.00	29.36
ATOM	1209	OE2	GLU	150	28.154	12.507	26.322	1.00	31.37
ATOM	1210	C	GLU	150	24.571	16.189	23.211	1.00	24.19
ATOM	1211	O	GLU	150	23.807	15.500	22.529	1.00	24.28
ATOM	1212	N	GLU	151	24.187	17.300	23.833	1.00	23.86
ATOM	1213	CA	GLU	151	22.818	17.787	23.757	1.00	23.65
ATOM	1214	CB	GLU	151	22.595	18.871	24.816	1.00	23.47
ATOM	1215	CG	GLU	151	22.812	18.336	26.238	1.00	23.24
ATOM	1216	CD	GLU	151	22.835	19.420	27.300	1.00	25.20
ATOM	1217	OE1	GLU	151	23.196	20.573	26.977	1.00	25.28
ATOM	1218	OE2	GLU	151	22.505	19.111	28.466	1.00	25.81
ATOM	1219	C	GLU	151	22.524	18.311	22.358	1.00	24.05
ATOM	1220	O	GLU	151	21.432	18.113	21.833	1.00	22.27
ATOM	1221	N	ILE	152	23.510	18.968	21.751	1.00	23.71
ATOM	1222	CA	ILE	152	23.342	19.487	20.406	1.00	24.39
ATOM	1223	CB	ILE	152	24.538	20.358	19.996	1.00	26.20
ATOM	1224	CG2	ILE	152	24.545	20.559	18.484	1.00	27.07
ATOM	1225	CG1	ILE	152	24.461	21.699	20.732	1.00	27.68
ATOM	1226	CD1	ILE	152	25.778	22.469	20.758	1.00	32.87
ATOM	1227	C	ILE	152	23.208	18.318	19.440	1.00	24.33
ATOM	1228	O	ILE	152	22.394	18.346	18.515	1.00	24.36
ATOM	1229	N	ALA	153	24.007	17.282	19.666	1.00	22.40
ATOM	1230	CA	ALA	153	23.968	16.097	18.821	1.00	21.95
ATOM	1231	CB	ALA	153	25.004	15.076	19.311	1.00	20.15
ATOM	1232	C	ALA	153	22.578	15.471	18.836	1.00	19.88
ATOM	1233	O	ALA	153	21.965	15.238	17.788	1.00	20.80
ATOM	1234	N	LEU	154	22.092	15.199	20.037	1.00	19.09
ATOM	1235	CA	LEU	154	20.794	14.573	20.222	1.00	21.33
ATOM	1236	CB	LEU	154	20.604	14.206	21.699	1.00	21.40
ATOM	1237	CG	LEU	154	21.616	13.184	22.230	1.00	24.62
ATOM	1238	CD1	LEU	154	21.415	12.961	23.728	1.00	25.79
ATOM	1239	CD2	LEU	154	21.448	11.878	21.472	1.00	25.80
ATOM	1240	C	LEU	154	19.653	15.456	19.730	1.00	21.75
ATOM	1241	O	LEU	154	18.742	14.979	19.044	1.00	20.76
ATOM	1242	N	PHE	155	19.706	16.744	20.061	1.00	21.95
ATOM	1243	CA	PHE	155	18.662	17.654	19.621	1.00	23.38
ATOM	1244	CB	PHE	155	18.826	19.038	20.250	1.00	22.84
ATOM	1245	CG	PHE	155	17.755	20.007	19.841	1.00	24.22

ATOM	1246	CD1	PHE	155	16.419	19.737	20.107	1.00	25.61
ATOM	1247	CD2	PHE	155	18.077	21.187	19.186	1.00	24.20
ATOM	1248	CE1	PHE	155	15.415	20.636	19.723	1.00	25.64
ATOM	1249	CE2	PHE	155	17.087	22.088	18.800	1.00	24.91
ATOM	1250	CZ	PHE	155	15.753	21.812	19.069	1.00	24.00
ATOM	1251	C	PHE	155	18.654	17.792	18.104	1.00	22.70
ATOM	1252	O	PHE	155	17.595	17.740	17.481	1.00	23.42
ATOM	1253	N	SER	156	19.824	17.967	17.502	1.00	22.39
ATOM	1254	CA	SER	156	19.873	18.105	16.053	1.00	21.92
ATOM	1255	CB	SER	156	21.308	18.330	15.565	1.00	23.31
ATOM	1256	OG	SER	156	22.097	17.163	15.712	1.00	21.35
ATOM	1257	C	SER	156	19.290	16.853	15.407	1.00	20.69
ATOM	1258	O	SER	156	18.632	16.939	14.378	1.00	21.06
ATOM	1259	N	SER	157	19.508	15.692	16.020	1.00	19.99
ATOM	1260	CA	SER	157	18.974	14.456	15.462	1.00	20.74
ATOM	1261	CB	SER	157	19.609	13.232	16.139	1.00	20.43
ATOM	1262	OG	SER	157	19.026	12.965	17.405	1.00	22.34
ATOM	1263	C	SER	157	17.443	14.403	15.596	1.00	21.96
ATOM	1264	O	SER	157	16.759	13.833	14.739	1.00	20.32
ATOM	1265	N	ALA	158	16.907	14.994	16.663	1.00	21.59
ATOM	1266	CA	ALA	158	15.453	15.015	16.866	1.00	23.00
ATOM	1267	CB	ALA	158	15.111	15.494	18.284	1.00	22.43
ATOM	1268	C	ALA	158	14.815	15.939	15.837	1.00	22.79
ATOM	1269	O	ALA	158	13.707	15.690	15.366	1.00	24.41
ATOM	1270	N	VAL	159	15.519	17.012	15.494	1.00	22.53
ATOM	1271	CA	VAL	159	15.037	17.965	14.497	1.00	21.80
ATOM	1272	CB	VAL	159	15.997	19.175	14.393	1.00	21.36
ATOM	1273	CG1	VAL	159	15.670	20.003	13.162	1.00	23.95
ATOM	1274	CG2	VAL	159	15.877	20.036	15.649	1.00	19.81
ATOM	1275	C	VAL	159	14.945	17.257	13.143	1.00	22.32
ATOM	1276	O	VAL	159	13.981	17.434	12.390	1.00	22.54
ATOM	1277	N	LEU	160	15.946	16.429	12.861	1.00	20.50
ATOM	1278	CA	LEU	160	16.011	15.661	11.622	1.00	21.56
ATOM	1279	CB	LEU	160	17.416	15.067	11.443	1.00	18.74
ATOM	1280	CG	LEU	160	17.565	14.114	10.252	1.00	20.46
ATOM	1281	CD1	LEU	160	17.342	14.880	8.962	1.00	23.67
ATOM	1282	CD2	LEU	160	18.944	13.466	10.269	1.00	22.07
ATOM	1283	C	LEU	160	14.988	14.523	11.574	1.00	22.22
ATOM	1284	O	LEU	160	14.305	14.336	10.569	1.00	23.99
ATOM	1285	N	ILE	161	14.906	13.753	12.654	1.00	24.28
ATOM	1286	CA	ILE	161	13.982	12.622	12.723	1.00	24.95
ATOM	1287	CB	ILE	161	14.492	11.534	13.712	1.00	25.36
ATOM	1288	CG2	ILE	161	13.739	10.234	13.494	1.00	24.65
ATOM	1289	CG1	ILE	161	15.993	11.289	13.515	1.00	29.20
ATOM	1290	CD1	ILE	161	16.372	10.830	12.152	1.00	31.88
ATOM	1291	C	ILE	161	12.632	13.136	13.203	1.00	23.52
ATOM	1292	O	ILE	161	12.214	12.852	14.327	1.00	22.05
ATOM	1293	N	SER	162	11.966	13.909	12.347	1.00	23.68
ATOM	1294	CA	SER	162	10.671	14.482	12.681	1.00	24.76
ATOM	1295	CB	SER	162	10.612	15.946	12.264	1.00	23.48
ATOM	1296	OG	SER	162	9.274	16.413	12.349	1.00	27.54
ATOM	1297	C	SER	162	9.514	13.742	12.030	1.00	25.92
ATOM	1298	O	SER	162	9.393	13.707	10.810	1.00	23.88
ATOM	1299	N	PRO	163	8.630	13.154	12.848	1.00	28.81
ATOM	1300	CD	PRO	163	8.685	13.100	14.321	1.00	28.18
ATOM	1301	CA	PRO	163	7.477	12.411	12.333	1.00	29.09
ATOM	1302	CB	PRO	163	7.018	11.612	13.546	1.00	28.39
ATOM	1303	CG	PRO	163	7.318	12.553	14.684	1.00	29.92
ATOM	1304	C	PRO	163	6.375	13.312	11.786	1.00	30.74
ATOM	1305	O	PRO	163	5.354	12.824	11.297	1.00	31.15
ATOM	1306	N	ASP	164	6.586	14.624	11.851	1.00	31.09
ATOM	1307	CA	ASP	164	5.582	15.563	11.371	1.00	32.86
ATOM	1308	CB	ASP	164	5.494	16.768	12.309	1.00	35.68
ATOM	1309	CG	ASP	164	5.004	16.383	13.697	1.00	41.26
ATOM	1310	OD1	ASP	164	3.928	15.754	13.790	1.00	42.32
ATOM	1311	OD2	ASP	164	5.691	16.704	14.692	1.00	44.22
ATOM	1312	C	ASP	164	5.788	16.038	9.942	1.00	31.89
ATOM	1313	O	ASP	164	4.929	16.727	9.394	1.00	31.96
ATOM	1314	N	ARG	165	6.910	15.665	9.333	1.00	29.36
ATOM	1315	CA	ARG	165	7.184	16.073	7.963	1.00	28.58
ATOM	1316	CB	ARG	165	8.525	15.507	7.477	1.00	25.79
ATOM	1317	CG	ARG	165	9.732	15.898	8.313	1.00	24.11
ATOM	1318	CD	ARG	165	9.861	17.404	8.460	1.00	20.61
ATOM	1319	NE	ARG	165	11.169	17.760	8.990	1.00	22.12
ATOM	1320	CZ	ARG	165	11.512	18.971	9.415	1.00	22.71
ATOM	1321	NH1	ARG	165	10.641	19.972	9.383	1.00	21.83
ATOM	1322	NH2	ARG	165	12.734	19.177	9.883	1.00	22.67
ATOM	1323	C	ARG	165	6.068	15.546	7.076	1.00	30.34
ATOM	1324	O	ARG	165	5.655	14.396	7.207	1.00	31.07
ATOM	1325	N	ALA	166	5.575	16.381	6.171	1.00	30.71
ATOM	1326	CA	ALA	166	4.507	15.945	5.287	1.00	30.26

ATOM	1327	CB	ALA	166	3.891	17.146	4.567	1.00	31.74
ATOM	1328	C	ALA	166	5.051	14.946	4.276	1.00	28.73
ATOM	1329	O	ALA	166	6.240	14.961	3.950	1.00	26.64
ATOM	1330	N	TRP	167	4.166	14.070	3.806	1.00	28.10
ATOM	1331	CA	TRP	167	4.475	13.046	2.806	1.00	27.46
ATOM	1332	CB	TRP	167	5.309	13.631	1.650	1.00	28.13
ATOM	1333	CG	TRP	167	4.811	14.960	1.098	1.00	32.39
ATOM	1334	CD2	TRP	167	3.672	15.177	0.245	1.00	31.61
ATOM	1335	CE2	TRP	167	3.616	16.560	-0.035	1.00	32.63
ATOM	1336	CE3	TRP	167	2.697	14.336	-0.307	1.00	31.53
ATOM	1337	CD1	TRP	167	5.378	16.192	1.292	1.00	33.04
ATOM	1338	NE1	TRP	167	4.666	17.155	0.614	1.00	33.34
ATOM	1339	CZ2	TRP	167	2.620	17.123	-0.847	1.00	32.95
ATOM	1340	CZ3	TRP	167	1.702	14.899	-1.121	1.00	31.83
ATOM	1341	CH2	TRP	167	1.675	16.277	-1.379	1.00	32.36
ATOM	1342	C	TRP	167	5.172	11.789	3.327	1.00	27.06
ATOM	1343	O	TRP	167	5.413	10.863	2.550	1.00	27.23
ATOM	1344	N	LEU	168	5.507	11.737	4.617	1.00	26.83
ATOM	1345	CA	LEU	168	6.161	10.537	5.145	1.00	26.56
ATOM	1346	CB	LEU	168	6.521	10.703	6.633	1.00	27.73
ATOM	1347	CG	LEU	168	7.684	11.644	7.009	1.00	26.59
ATOM	1348	CD1	LEU	168	7.798	11.758	8.529	1.00	25.28
ATOM	1349	CD2	LEU	168	8.982	11.124	6.417	1.00	25.28
ATOM	1350	C	LEU	168	5.217	9.347	4.973	1.00	28.20
ATOM	1351	O	LEU	168	4.022	9.457	5.241	1.00	26.68
ATOM	1352	N	LEU	169	5.755	8.219	4.513	1.00	28.02
ATOM	1353	CA	LEU	169	4.954	7.016	4.307	1.00	28.10
ATOM	1354	CB	LEU	169	5.588	6.132	3.231	1.00	27.55
ATOM	1355	CG	LEU	169	5.571	6.687	1.802	1.00	29.51
ATOM	1356	CD1	LEU	169	6.406	5.802	0.879	1.00	26.49
ATOM	1357	CD2	LEU	169	4.130	6.785	1.319	1.00	26.84
ATOM	1358	C	LEU	169	4.785	6.216	5.593	1.00	29.45
ATOM	1359	O	LEU	169	3.754	5.582	5.800	1.00	30.01
ATOM	1360	N	GLU	170	5.801	6.237	6.452	1.00	29.04
ATOM	1361	CA	GLU	170	5.736	5.518	7.721	1.00	29.15
ATOM	1362	CB	GLU	170	6.684	4.315	7.706	1.00	29.47
ATOM	1363	CG	GLU	170	6.321	3.256	6.672	1.00	32.25
ATOM	1364	CD	GLU	170	7.296	2.095	6.659	1.00	32.48
ATOM	1365	OE1	GLU	170	8.494	2.323	6.391	1.00	35.86
ATOM	1366	OE2	GLU	170	6.866	0.954	6.918	1.00	33.16
ATOM	1367	C	GLU	170	6.106	6.453	8.863	1.00	28.40
ATOM	1368	O	GLU	170	7.150	6.297	9.493	1.00	26.92
ATOM	1369	N	PRO	171	5.241	7.440	9.148	1.00	29.50
ATOM	1370	CD	PRO	171	3.953	7.686	8.474	1.00	28.57
ATOM	1371	CA	PRO	171	5.467	8.416	10.217	1.00	29.67
ATOM	1372	CB	PRO	171	4.238	9.320	10.125	1.00	30.97
ATOM	1373	CG	PRO	171	3.174	8.408	9.536	1.00	29.77
ATOM	1374	C	PRO	171	5.652	7.816	11.610	1.00	31.30
ATOM	1375	O	PRO	171	6.520	8.259	12.371	1.00	28.88
ATOM	1376	N	ARG	172	4.838	6.815	11.940	1.00	31.06
ATOM	1377	CA	ARG	172	4.915	6.153	13.240	1.00	32.55
ATOM	1378	CB	ARG	172	3.916	4.992	13.299	1.00	36.17
ATOM	1379	CG	ARG	172	2.639	5.296	14.065	1.00	42.42
ATOM	1380	CD	ARG	172	2.802	4.986	15.561	1.00	49.54
ATOM	1381	NE	ARG	172	3.861	5.774	16.202	1.00	53.35
ATOM	1382	CZ	ARG	172	4.305	5.573	17.443	1.00	55.25
ATOM	1383	NH1	ARG	172	3.788	4.604	18.192	1.00	56.19
ATOM	1384	NH2	ARG	172	5.268	6.342	17.941	1.00	56.24
ATOM	1385	C	ARG	172	6.319	5.637	13.552	1.00	31.45
ATOM	1386	O	ARG	172	6.764	5.702	14.702	1.00	30.68
ATOM	1387	N	LYS	173	7.010	5.117	12.540	1.00	29.22
ATOM	1388	CA	LYS	173	8.363	4.615	12.743	1.00	29.66
ATOM	1389	CB	LYS	173	8.861	3.870	11.503	1.00	32.78
ATOM	1390	CG	LYS	173	8.200	2.513	11.305	1.00	37.00
ATOM	1391	CD	LYS	173	8.782	1.776	10.116	1.00	39.09
ATOM	1392	CE	LYS	173	8.072	0.449	9.888	1.00	41.03
ATOM	1393	NZ	LYS	173	8.678	-0.294	8.745	1.00	43.13
ATOM	1394	C	LYS	173	9.300	5.768	13.076	1.00	28.29
ATOM	1395	O	LYS	173	10.207	5.625	13.894	1.00	26.75
ATOM	1396	N	VAL	174	9.082	6.913	12.441	1.00	26.90
ATOM	1397	CA	VAL	174	9.903	8.085	12.713	1.00	25.57
ATOM	1398	CB	VAL	174	9.616	9.215	11.709	1.00	23.33
ATOM	1399	CG1	VAL	174	10.401	10.474	12.096	1.00	20.63
ATOM	1400	CG2	VAL	174	9.999	8.758	10.303	1.00	22.21
ATOM	1401	C	VAL	174	9.587	8.575	14.122	1.00	26.24
ATOM	1402	O	VAL	174	10.484	8.917	14.889	1.00	24.66
ATOM	1403	N	GLN	175	8.303	8.603	14.458	1.00	27.11
ATOM	1404	CA	GLN	175	7.869	9.040	15.779	1.00	28.66
ATOM	1405	CB	GLN	175	6.339	8.967	15.878	1.00	31.02
ATOM	1406	CG	GLN	175	5.779	9.114	17.286	1.00	38.22
ATOM	1407	CD	GLN	175	4.257	9.212	17.301	1.00	42.67

ATOM	1408	OE1	GLN	175	3.570	8.514	16.550	1.00	45.50
ATOM	1409	NE2	GLN	175	3.723	10.073	18.164	1.00	43.62
ATOM	1410	C	GLN	175	8.500	8.188	16.875	1.00	28.75
ATOM	1411	O	GLN	175	8.945	8.712	17.901	1.00	26.15
ATOM	1412	N	LYS	176	8.541	6.876	16.654	1.00	28.86
ATOM	1413	CA	LYS	176	9.107	5.956	17.636	1.00	28.72
ATOM	1414	CB	LYS	176	8.919	4.505	17.183	1.00	31.92
ATOM	1415	CG	LYS	176	7.473	4.016	17.228	1.00	34.30
ATOM	1416	CD	LYS	176	7.364	2.603	16.658	1.00	37.65
ATOM	1417	CE	LYS	176	5.916	2.139	16.565	1.00	40.91
ATOM	1418	NZ	LYS	176	5.250	2.029	17.897	1.00	43.69
ATOM	1419	C	LYS	176	10.584	6.223	17.897	1.00	28.09
ATOM	1420	O	LYS	176	11.030	6.193	19.046	1.00	26.98
ATOM	1421	N	LEU	177	11.343	6.483	16.836	1.00	26.02
ATOM	1422	CA	LEU	177	12.765	6.759	16.994	1.00	25.81
ATOM	1423	CB	LEU	177	13.484	6.723	15.635	1.00	24.35
ATOM	1424	CG	LEU	177	14.977	7.090	15.579	1.00	22.01
ATOM	1425	CD1	LEU	177	15.766	6.331	16.644	1.00	22.19
ATOM	1426	CD2	LEU	177	15.518	6.775	14.192	1.00	21.74
ATOM	1427	C	LEU	177	12.968	8.114	17.662	1.00	26.28
ATOM	1428	O	LEU	177	13.832	8.258	18.531	1.00	25.96
ATOM	1429	N	GLN	178	12.173	9.107	17.272	1.00	25.47
ATOM	1430	CA	GLN	178	12.321	10.429	17.860	1.00	25.14
ATOM	1431	CB	GLN	178	11.416	11.457	17.182	1.00	24.25
ATOM	1432	CG	GLN	178	11.846	12.882	17.499	1.00	23.94
ATOM	1433	CD	GLN	178	10.808	13.935	17.145	1.00	25.80
ATOM	1434	OE1	GLN	178	11.140	14.977	16.579	1.00	26.74
ATOM	1435	NE2	GLN	178	9.559	13.683	17.498	1.00	22.56
ATOM	1436	C	GLN	178	12.018	10.428	19.357	1.00	26.38
ATOM	1437	O	GLN	178	12.634	11.181	20.117	1.00	25.08
ATOM	1438	N	GLU	179	11.068	9.599	19.785	1.00	26.53
ATOM	1439	CA	GLU	179	10.722	9.544	21.205	1.00	28.84
ATOM	1440	CB	GLU	179	9.459	8.701	21.434	1.00	31.20
ATOM	1441	CG	GLU	179	8.231	9.239	20.723	1.00	36.58
ATOM	1442	CD	GLU	179	6.954	8.494	21.087	1.00	41.47
ATOM	1443	OE1	GLU	179	5.955	8.650	20.353	1.00	43.13
ATOM	1444	OE2	GLU	179	6.948	7.763	22.104	1.00	43.96
ATOM	1445	C	GLU	179	11.880	8.974	22.015	1.00	26.71
ATOM	1446	O	GLU	179	12.134	9.414	23.136	1.00	26.95
ATOM	1447	N	LYS	180	12.577	7.993	21.451	1.00	25.60
ATOM	1448	CA	LYS	180	13.710	7.394	22.141	1.00	25.20
ATOM	1449	CB	LYS	180	14.201	6.153	21.391	1.00	26.31
ATOM	1450	CG	LYS	180	13.223	4.981	21.476	1.00	26.70
ATOM	1451	CD	LYS	180	13.546	3.909	20.452	1.00	26.50
ATOM	1452	CE	LYS	180	12.394	2.906	20.308	1.00	26.04
ATOM	1453	NZ	LYS	180	12.689	1.913	19.246	1.00	24.63
ATOM	1454	C	LYS	180	14.811	8.434	22.237	1.00	25.02
ATOM	1455	O	LYS	180	15.505	8.520	23.244	1.00	23.42
ATOM	1456	N	ILE	181	14.955	9.242	21.189	1.00	25.84
ATOM	1457	CA	ILE	181	15.969	10.291	21.179	1.00	23.07
ATOM	1458	CB	ILE	181	16.073	10.948	19.784	1.00	22.59
ATOM	1459	CG2	ILE	181	16.997	12.160	19.837	1.00	21.40
ATOM	1460	CG1	ILE	181	16.612	9.926	18.773	1.00	22.13
ATOM	1461	CD1	ILE	181	16.648	10.429	17.343	1.00	20.82
ATOM	1462	C	ILE	181	15.659	11.359	22.233	1.00	24.68
ATOM	1463	O	ILE	181	16.544	11.768	22.988	1.00	24.27
ATOM	1464	N	TYR	182	14.406	11.803	22.292	1.00	24.89
ATOM	1465	CA	TYR	182	14.010	12.821	23.263	1.00	25.67
ATOM	1466	CB	TYR	182	12.563	13.254	23.019	1.00	27.04
ATOM	1467	CG	TYR	182	12.440	14.408	22.052	1.00	28.95
ATOM	1468	CD1	TYR	182	11.386	14.474	21.145	1.00	29.65
ATOM	1469	CE1	TYR	182	11.270	15.540	20.250	1.00	28.75
ATOM	1470	CD2	TYR	182	13.376	15.437	22.049	1.00	28.12
ATOM	1471	CE2	TYR	182	13.271	16.506	21.165	1.00	30.56
ATOM	1472	CZ	TYR	182	12.216	16.550	20.266	1.00	28.99
ATOM	1473	OH	TYR	182	12.119	17.595	19.381	1.00	29.53
ATOM	1474	C	TYR	182	14.166	12.328	24.695	1.00	26.66
ATOM	1475	O	TYR	182	14.539	13.093	25.586	1.00	26.29
ATOM	1476	N	PHE	183	13.879	11.050	24.910	1.00	26.50
ATOM	1477	CA	PHE	183	14.008	10.457	26.232	1.00	29.79
ATOM	1478	CB	PHE	183	13.388	9.057	26.249	1.00	34.77
ATOM	1479	CG	PHE	183	11.913	9.045	26.597	1.00	44.65
ATOM	1480	CD1	PHE	183	11.105	7.963	26.237	1.00	48.06
ATOM	1481	CD2	PHE	183	11.337	10.097	27.321	1.00	47.29
ATOM	1482	CE1	PHE	183	9.739	7.929	26.592	1.00	49.51
ATOM	1483	CE2	PHE	183	9.976	10.071	27.681	1.00	48.55
ATOM	1484	CZ	PHE	183	9.179	8.985	27.315	1.00	48.81
ATOM	1485	C	PHE	183	15.483	10.397	26.619	1.00	28.13
ATOM	1486	O	PHE	183	15.826	10.610	27.771	1.00	27.21
ATOM	1487	N	ALA	184	16.351	10.117	25.650	1.00	28.03
ATOM	1488	CA	ALA	184	17.785	10.060	25.907	1.00	26.92

ATOM	1489	CB	ALA	184	18.519	9.527	24.684	1.00	26.34
ATOM	1490	C	ALA	184	18.291	11.460	26.240	1.00	25.39
ATOM	1491	O	ALA	184	19.044	11.658	27.196	1.00	25.22
ATOM	1492	N	LEU	185	17.862	12.429	25.441	1.00	24.98
ATOM	1493	CA	LEU	185	18.268	13.816	25.620	1.00	24.30
ATOM	1494	CB	LEU	185	17.704	14.671	24.488	1.00	24.30
ATOM	1495	CG	LEU	185	17.940	16.182	24.573	1.00	24.55
ATOM	1496	CD1	LEU	185	19.449	16.479	24.607	1.00	21.33
ATOM	1497	CD2	LEU	185	17.283	16.860	23.367	1.00	22.54
ATOM	1498	C	LEU	185	17.821	14.392	26.957	1.00	24.99
ATOM	1499	O	LEU	185	18.537	15.178	27.569	1.00	24.67
ATOM	1500	N	GLN	186	16.631	14.011	27.400	1.00	25.81
ATOM	1501	CA	GLN	186	16.103	14.506	28.660	1.00	26.62
ATOM	1502	CB	GLN	186	14.694	13.966	28.876	1.00	30.90
ATOM	1503	CG	GLN	186	13.997	14.508	30.094	1.00	36.75
ATOM	1504	CD	GLN	186	12.629	13.896	30.263	1.00	43.23
ATOM	1505	OE1	GLN	186	12.491	12.666	30.304	1.00	46.44
ATOM	1506	NE2	GLN	186	11.602	14.744	30.354	1.00	43.40
ATOM	1507	C	GLN	186	17.006	14.073	29.807	1.00	27.38
ATOM	1508	O	GLN	186	17.212	14.824	30.762	1.00	27.01
ATOM	1509	N	HIS	187	17.544	12.860	29.715	1.00	27.90
ATOM	1510	CA	HIS	187	18.433	12.356	30.756	1.00	27.79
ATOM	1511	CB	HIS	187	18.610	10.846	30.604	1.00	28.15
ATOM	1512	CG	HIS	187	17.409	10.064	31.028	1.00	29.94
ATOM	1513	CD2	HIS	187	16.329	9.642	30.330	1.00	31.20
ATOM	1514	ND1	HIS	187	17.185	9.695	32.337	1.00	32.49
ATOM	1515	CE1	HIS	187	16.019	9.083	32.428	1.00	30.69
ATOM	1516	NE2	HIS	187	15.478	9.038	31.225	1.00	32.71
ATOM	1517	C	HIS	187	19.785	13.066	30.724	1.00	27.63
ATOM	1518	O	HIS	187	20.312	13.450	31.771	1.00	25.57
ATOM	1519	N	VAL	188	20.337	13.251	29.526	1.00	27.19
ATOM	1520	CA	VAL	188	21.623	13.932	29.371	1.00	26.76
ATOM	1521	CB	VAL	188	22.032	14.045	27.876	1.00	27.81
ATOM	1522	CG1	VAL	188	23.281	14.923	27.734	1.00	25.30
ATOM	1523	CG2	VAL	188	22.283	12.657	27.301	1.00	26.52
ATOM	1524	C	VAL	188	21.545	15.341	29.954	1.00	27.08
ATOM	1525	O	VAL	188	22.460	15.801	30.639	1.00	27.95
ATOM	1526	N	ILE	189	20.444	16.023	29.675	1.00	26.81
ATOM	1527	CA	ILE	189	20.243	17.382	30.156	1.00	28.56
ATOM	1528	CB	ILE	189	18.865	17.902	29.700	1.00	27.38
ATOM	1529	CG2	ILE	189	18.428	19.099	30.549	1.00	27.87
ATOM	1530	CG1	ILE	189	18.940	18.263	28.213	1.00	25.31
ATOM	1531	CD1	ILE	189	17.612	18.583	27.585	1.00	23.03
ATOM	1532	C	ILE	189	20.381	17.482	31.675	1.00	29.59
ATOM	1533	O	ILE	189	20.810	18.504	32.205	1.00	28.17
ATOM	1534	N	GLN	190	20.025	16.413	32.374	1.00	31.73
ATOM	1535	CA	GLN	190	20.130	16.401	33.824	1.00	34.66
ATOM	1536	CB	GLN	190	19.517	15.115	34.383	1.00	35.71
ATOM	1537	CG	GLN	190	18.181	14.749	33.767	1.00	36.32
ATOM	1538	CD	GLN	190	17.525	13.575	34.469	1.00	37.87
ATOM	1539	OE1	GLN	190	18.207	12.705	35.008	1.00	37.94
ATOM	1540	NE2	GLN	190	16.195	13.537	34.453	1.00	37.69
ATOM	1541	C	GLN	190	21.589	16.522	34.282	1.00	36.42
ATOM	1542	O	GLN	190	21.864	17.088	35.341	1.00	37.31
ATOM	1543	N	LYS	191	22.522	15.995	33.491	1.00	36.35
ATOM	1544	CA	LYS	191	23.944	16.060	33.849	1.00	38.86
ATOM	1545	CB	LYS	191	24.816	15.373	32.798	1.00	36.60
ATOM	1546	CG	LYS	191	24.892	13.887	32.917	1.00	34.28
ATOM	1547	CD	LYS	191	26.075	13.357	32.132	1.00	33.89
ATOM	1548	CE	LYS	191	25.937	13.646	30.650	1.00	32.20
ATOM	1549	NZ	LYS	191	27.090	13.103	29.891	1.00	33.09
ATOM	1550	C	LYS	191	24.424	17.491	33.962	1.00	40.84
ATOM	1551	O	LYS	191	25.233	17.835	34.822	1.00	40.86
ATOM	1552	N	ASN	192	23.928	18.318	33.056	1.00	43.43
ATOM	1553	CA	ASN	192	24.297	19.714	33.003	1.00	45.38
ATOM	1554	CB	ASN	192	24.548	20.071	31.541	1.00	44.67
ATOM	1555	CG	ASN	192	25.345	18.985	30.817	1.00	44.92
ATOM	1556	OD1	ASN	192	26.513	18.751	31.126	1.00	42.55
ATOM	1557	ND2	ASN	192	24.705	18.301	29.870	1.00	43.86
ATOM	1558	C	ASN	192	23.151	20.518	33.607	1.00	47.90
ATOM	1559	O	ASN	192	22.728	20.250	34.732	1.00	50.09
ATOM	1560	N	HIS	193	22.653	21.490	32.859	1.00	48.81
ATOM	1561	CA	HIS	193	21.548	22.351	33.281	1.00	51.29
ATOM	1562	CB	HIS	193	20.616	22.551	32.091	1.00	49.68
ATOM	1563	CG	HIS	193	21.321	22.468	30.777	1.00	49.19
ATOM	1564	CD2	HIS	193	21.274	21.535	29.798	1.00	47.56
ATOM	1565	ND1	HIS	193	22.270	23.387	30.387	1.00	47.61
ATOM	1566	CE1	HIS	193	22.780	23.022	29.224	1.00	48.67
ATOM	1567	NE2	HIS	193	22.193	21.901	28.846	1.00	47.30
ATOM	1568	C	HIS	193	20.730	21.875	34.487	1.00	53.71
ATOM	1569	O	HIS	193	19.715	21.195	34.328	1.00	53.57

ATOM	1570	N	LEU	194	21.168	22.233	35.692	1.00	57.22
ATOM	1571	CA	LEU	194	20.433	21.852	36.897	1.00	60.04
ATOM	1572	CB	LEU	194	21.288	22.076	38.151	1.00	60.66
ATOM	1573	CG	LEU	194	20.990	21.191	39.372	1.00	61.69
ATOM	1574	CD1	LEU	194	19.593	21.481	39.902	1.00	61.58
ATOM	1575	CD2	LEU	194	21.127	19.716	38.987	1.00	60.81
ATOM	1576	C	LEU	194	19.240	22.797	36.874	1.00	61.24
ATOM	1577	O	LEU	194	19.397	23.968	36.530	1.00	61.98
ATOM	1578	N	ASP	195	18.059	22.304	37.242	1.00	62.55
ATOM	1579	CA	ASP	195	16.846	23.119	37.178	1.00	63.43
ATOM	1580	CB	ASP	195	17.019	24.440	37.937	1.00	66.10
ATOM	1581	CG	ASP	195	16.716	24.303	39.424	1.00	67.60
ATOM	1582	OD1	ASP	195	17.314	23.423	40.082	1.00	67.56
ATOM	1583	OD2	ASP	195	15.875	25.076	39.934	1.00	68.82
ATOM	1584	C	ASP	195	16.696	23.351	35.681	1.00	62.91
ATOM	1585	O	ASP	195	17.481	24.071	35.062	1.00	62.29
ATOM	1586	N	ASP	196	15.680	22.739	35.095	1.00	62.38
ATOM	1587	CA	ASP	196	15.525	22.819	33.661	1.00	61.54
ATOM	1588	CB	ASP	196	15.581	21.397	33.106	1.00	62.97
ATOM	1589	CG	ASP	196	14.499	20.508	33.693	1.00	63.92
ATOM	1590	OD1	ASP	196	13.365	20.512	33.165	1.00	63.95
ATOM	1591	OD2	ASP	196	14.777	19.817	34.697	1.00	64.35
ATOM	1592	C	ASP	196	14.350	23.545	33.028	1.00	60.76
ATOM	1593	O	ASP	196	14.171	24.758	33.190	1.00	59.34
ATOM	1594	N	GLU	197	13.572	22.747	32.298	1.00	58.84
ATOM	1595	CA	GLU	197	12.429	23.157	31.494	1.00	57.17
ATOM	1596	CB	GLU	197	11.960	24.576	31.830	1.00	59.78
ATOM	1597	CG	GLU	197	10.901	25.109	30.876	1.00	63.41
ATOM	1598	CD	GLU	197	10.666	26.601	31.023	1.00	66.17
ATOM	1599	OE1	GLU	197	9.831	27.144	30.268	1.00	67.86
ATOM	1600	OE2	GLU	197	11.313	27.231	31.888	1.00	68.19
ATOM	1601	C	GLU	197	13.138	23.163	30.147	1.00	53.54
ATOM	1602	O	GLU	197	12.537	23.364	29.092	1.00	54.00
ATOM	1603	N	THR	198	14.446	22.924	30.229	1.00	48.95
ATOM	1604	CA	THR	198	15.345	22.910	29.088	1.00	43.99
ATOM	1605	CB	THR	198	16.731	22.376	29.499	1.00	43.60
ATOM	1606	OG1	THR	198	17.251	23.185	30.559	1.00	42.61
ATOM	1607	CG2	THR	198	17.699	22.422	28.318	1.00	43.36
ATOM	1608	C	THR	198	14.842	22.125	27.889	1.00	39.98
ATOM	1609	O	THR	198	14.772	22.665	26.790	1.00	39.06
ATOM	1610	N	LEU	199	14.497	20.857	28.084	1.00	37.03
ATOM	1611	CA	LEU	199	14.009	20.057	26.966	1.00	35.00
ATOM	1612	CB	LEU	199	13.650	18.639	27.414	1.00	34.87
ATOM	1613	CG	LEU	199	13.972	17.518	26.418	1.00	34.97
ATOM	1614	CD1	LEU	199	13.114	16.299	26.728	1.00	34.01
ATOM	1615	CD2	LEU	199	13.729	17.980	25.004	1.00	33.06
ATOM	1616	C	LEU	199	12.774	20.725	26.362	1.00	33.27
ATOM	1617	O	LEU	199	12.668	20.860	25.148	1.00	31.34
ATOM	1618	N	ALA	200	11.849	21.147	27.219	1.00	32.76
ATOM	1619	CA	ALA	200	10.625	21.804	26.763	1.00	33.19
ATOM	1620	CB	ALA	200	9.706	22.120	27.963	1.00	32.22
ATOM	1621	C	ALA	200	10.956	23.084	26.002	1.00	32.43
ATOM	1622	O	ALA	200	10.341	23.380	24.977	1.00	31.79
ATOM	1623	N	LYS	201	11.931	23.841	26.497	1.00	32.28
ATOM	1624	CA	LYS	201	12.327	25.084	25.838	1.00	32.01
ATOM	1625	CB	LYS	201	13.342	25.854	26.682	1.00	35.09
ATOM	1626	CG	LYS	201	12.853	26.322	28.036	1.00	36.56
ATOM	1627	CD	LYS	201	13.903	27.242	28.652	1.00	40.79
ATOM	1628	CE	LYS	201	13.616	27.553	30.107	1.00	43.94
ATOM	1629	NZ	LYS	201	14.677	28.430	30.671	1.00	47.03
ATOM	1630	C	LYS	201	12.946	24.787	24.480	1.00	30.91
ATOM	1631	O	LYS	201	12.775	25.552	23.531	1.00	30.11
ATOM	1632	N	LEU	202	13.683	23.683	24.391	1.00	30.46
ATOM	1633	CA	LEU	202	14.307	23.297	23.129	1.00	29.29
ATOM	1634	CB	LEU	202	15.258	22.117	23.331	1.00	28.23
ATOM	1635	CG	LEU	202	16.633	22.426	23.923	1.00	29.50
ATOM	1636	CD1	LEU	202	17.429	21.126	24.055	1.00	27.57
ATOM	1637	CD2	LEU	202	17.367	23.417	23.022	1.00	27.80
ATOM	1638	C	LEU	202	13.224	22.906	22.138	1.00	28.85
ATOM	1639	O	LEU	202	13.181	23.399	21.011	1.00	30.02
ATOM	1640	N	ILE	203	12.348	22.011	22.567	1.00	28.20
ATOM	1641	CA	ILE	203	11.261	21.552	21.722	1.00	29.72
ATOM	1642	CB	ILE	203	10.370	20.553	22.498	1.00	30.66
ATOM	1643	CG2	ILE	203	9.101	20.248	21.709	1.00	31.62
ATOM	1644	CG1	ILE	203	11.165	19.271	22.774	1.00	33.22
ATOM	1645	CD1	ILE	203	10.477	18.296	23.714	1.00	33.21
ATOM	1646	C	ILE	203	10.415	22.729	21.217	1.00	28.90
ATOM	1647	O	ILE	203	9.962	22.734	20.073	1.00	26.56
ATOM	1648	N	ALA	204	10.228	23.733	22.070	1.00	28.33
ATOM	1649	CA	ALA	204	9.434	24.904	21.716	1.00	28.52
ATOM	1650	CB	ALA	204	9.188	25.761	22.948	1.00	29.61

ATOM	1651	C	ALA	204	10.076	25.754	20.629	1.00	29.35
ATOM	1652	O	ALA	204	9.423	26.622	20.054	1.00	28.72
ATOM	1653	N	LYS	205	11.354	25.520	20.351	1.00	27.27
ATOM	1654	CA	LYS	205	12.039	26.293	19.326	1.00	27.82
ATOM	1655	CB	LYS	205	13.525	26.443	19.674	1.00	28.06
ATOM	1656	CG	LYS	205	13.779	27.246	20.941	1.00	31.35
ATOM	1657	CD	LYS	205	15.270	27.343	21.249	1.00	32.78
ATOM	1658	CE	LYS	205	15.505	27.938	22.624	1.00	36.42
ATOM	1659	NZ	LYS	205	14.840	29.262	22.784	1.00	40.34
ATOM	1660	C	LYS	205	11.894	25.657	17.945	1.00	27.11
ATOM	1661	O	LYS	205	12.205	26.284	16.938	1.00	28.06
ATOM	1662	N	ILE	206	11.417	24.418	17.897	1.00	27.34
ATOM	1663	CA	ILE	206	11.256	23.725	16.621	1.00	28.94
ATOM	1664	CB	ILE	206	10.453	22.417	16.794	1.00	29.50
ATOM	1665	CG2	ILE	206	10.159	21.801	15.429	1.00	31.00
ATOM	1666	CG1	ILE	206	11.214	21.447	17.703	1.00	28.15
ATOM	1667	CD1	ILE	206	12.423	20.830	17.088	1.00	28.61
ATOM	1668	C	ILE	206	10.562	24.590	15.559	1.00	29.28
ATOM	1669	O	ILE	206	11.094	24.783	14.462	1.00	30.10
ATOM	1670	N	PRO	207	9.366	25.125	15.869	1.00	30.04
ATOM	1671	CD	PRO	207	8.554	24.973	17.089	1.00	29.62
ATOM	1672	CA	PRO	207	8.673	25.957	14.877	1.00	30.42
ATOM	1673	CB	PRO	207	7.365	26.337	15.582	1.00	31.19
ATOM	1674	CG	PRO	207	7.695	26.204	17.041	1.00	33.14
ATOM	1675	C	PRO	207	9.480	27.165	14.417	1.00	29.62
ATOM	1676	O	PRO	207	9.339	27.616	13.281	1.00	29.83
ATOM	1677	N	THR	208	10.339	27.675	15.290	1.00	26.85
ATOM	1678	CA	THR	208	11.162	28.819	14.935	1.00	28.12
ATOM	1679	CB	THR	208	11.856	29.396	16.159	1.00	29.03
ATOM	1680	OG1	THR	208	10.864	29.918	17.052	1.00	31.90
ATOM	1681	CG2	THR	208	12.821	30.506	15.751	1.00	29.68
ATOM	1682	C	THR	208	12.216	28.407	13.915	1.00	28.22
ATOM	1683	O	THR	208	12.463	29.113	12.944	1.00	28.12
ATOM	1684	N	ILE	209	12.830	27.252	14.142	1.00	26.44
ATOM	1685	CA	ILE	209	13.850	26.746	13.240	1.00	25.22
ATOM	1686	CB	ILE	209	14.375	25.383	13.732	1.00	23.83
ATOM	1687	CG2	ILE	209	15.308	24.776	12.693	1.00	23.71
ATOM	1688	CG1	ILE	209	15.079	25.568	15.081	1.00	21.30
ATOM	1689	CD1	ILE	209	15.644	24.294	15.685	1.00	21.88
ATOM	1690	C	ILE	209	13.256	26.602	11.842	1.00	23.64
ATOM	1691	O	ILE	209	13.884	26.965	10.847	1.00	24.10
ATOM	1692	N	THR	210	12.035	26.083	11.781	1.00	23.76
ATOM	1693	CA	THR	210	11.334	25.888	10.520	1.00	21.79
ATOM	1694	CB	THR	210	10.047	25.064	10.737	1.00	22.51
ATOM	1695	OG1	THR	210	10.397	23.748	11.173	1.00	21.60
ATOM	1696	CG2	THR	210	9.248	24.958	9.448	1.00	24.33
ATOM	1697	C	THR	210	10.974	27.202	9.825	1.00	22.08
ATOM	1698	O	THR	210	11.033	27.289	8.603	1.00	22.39
ATOM	1699	N	ALA	211	10.604	28.220	10.600	1.00	22.88
ATOM	1700	CA	ALA	211	10.239	29.526	10.037	1.00	22.29
ATOM	1701	CB	ALA	211	9.678	30.435	11.127	1.00	23.28
ATOM	1702	C	ALA	211	11.451	30.186	9.384	1.00	23.47
ATOM	1703	O	ALA	211	11.334	30.822	8.335	1.00	23.25
ATOM	1704	N	VAL	212	12.617	30.045	10.006	1.00	22.80
ATOM	1705	CA	VAL	212	13.824	30.627	9.433	1.00	23.37
ATOM	1706	CB	VAL	212	15.049	30.433	10.353	1.00	23.62
ATOM	1707	CG1	VAL	212	16.298	30.998	9.684	1.00	22.67
ATOM	1708	CG2	VAL	212	14.811	31.125	11.682	1.00	24.14
ATOM	1709	C	VAL	212	14.115	29.970	8.088	1.00	23.99
ATOM	1710	O	VAL	212	14.409	30.649	7.106	1.00	25.86
ATOM	1711	N	CYS	213	14.012	28.645	8.041	1.00	23.57
ATOM	1712	CA	CYS	213	14.284	27.910	6.814	1.00	25.76
ATOM	1713	CB	CYS	213	14.404	26.411	7.123	1.00	25.45
ATOM	1714	SG	CYS	213	15.842	26.040	8.202	1.00	29.19
ATOM	1715	C	CYS	213	13.259	28.167	5.704	1.00	27.48
ATOM	1716	O	CYS	213	13.613	28.194	4.521	1.00	26.56
ATOM	1717	N	ASN	214	11.994	28.358	6.063	1.00	28.96
ATOM	1718	CA	ASN	214	10.998	28.640	5.031	1.00	30.22
ATOM	1719	CB	ASN	214	9.573	28.612	5.592	1.00	32.61
ATOM	1720	CG	ASN	214	9.129	27.218	5.987	1.00	34.72
ATOM	1721	OD1	ASN	214	9.481	26.237	5.337	1.00	35.64
ATOM	1722	ND2	ASN	214	8.335	27.128	7.043	1.00	36.05
ATOM	1723	C	ASN	214	11.297	30.021	4.473	1.00	29.75
ATOM	1724	O	ASN	214	11.165	30.260	3.275	1.00	30.40
ATOM	1725	N	LEU	215	11.712	30.930	5.348	1.00	28.89
ATOM	1726	CA	LEU	215	12.033	32.278	4.909	1.00	27.73
ATOM	1727	CB	LEU	215	12.411	33.151	6.104	1.00	26.66
ATOM	1728	CG	LEU	215	12.531	34.649	5.816	1.00	28.15
ATOM	1729	CD1	LEU	215	11.296	35.147	5.064	1.00	29.37
ATOM	1730	CD2	LEU	215	12.699	35.393	7.124	1.00	29.37
ATOM	1731	C	LEU	215	13.179	32.197	3.904	1.00	27.61

ATOM	1732	O	LEU	215	13.206	32.939	2.918	1.00	27.88
ATOM	1733	N	HIS	216	14.119	31.284	4.150	1.00	26.67
ATOM	1734	CA	HIS	216	15.246	31.081	3.244	1.00	25.98
ATOM	1735	CB	HIS	216	16.177	29.982	3.777	1.00	26.15
ATOM	1736	CG	HIS	216	17.116	29.420	2.748	1.00	25.88
ATOM	1737	CD2	HIS	216	18.361	29.799	2.372	1.00	25.25
ATOM	1738	ND1	HIS	216	16.785	28.351	1.942	1.00	27.09
ATOM	1739	CE1	HIS	216	17.784	28.098	1.115	1.00	26.92
ATOM	1740	NE2	HIS	216	18.753	28.964	1.355	1.00	24.89
ATOM	1741	C	HIS	216	14.692	30.674	1.884	1.00	26.04
ATOM	1742	O	HIS	216	15.052	31.247	0.860	1.00	26.79
ATOM	1743	N	GLY	217	13.810	29.681	1.885	1.00	26.73
ATOM	1744	CA	GLY	217	13.220	29.223	0.641	1.00	28.62
ATOM	1745	C	GLY	217	12.537	30.359	-0.096	1.00	30.50
ATOM	1746	O	GLY	217	12.648	30.471	-1.314	1.00	30.23
ATOM	1747	N	GLU	218	11.829	31.209	0.644	1.00	33.00
ATOM	1748	CA	GLU	218	11.128	32.344	0.050	1.00	34.40
ATOM	1749	CB	GLU	218	10.279	33.050	1.110	1.00	37.30
ATOM	1750	CG	GLU	218	9.078	32.243	1.568	1.00	43.62
ATOM	1751	CD	GLU	218	8.375	32.862	2.765	1.00	48.13
ATOM	1752	OE1	GLU	218	8.082	34.077	2.718	1.00	50.14
ATOM	1753	OE2	GLU	218	8.108	32.131	3.750	1.00	50.72
ATOM	1754	C	GLU	218	12.092	33.338	-0.590	1.00	33.43
ATOM	1755	O	GLU	218	11.906	33.735	-1.735	1.00	33.17
ATOM	1756	N	LYS	219	13.120	33.742	0.151	1.00	33.47
ATOM	1757	CA	LYS	219	14.100	34.686	-0.368	1.00	33.64
ATOM	1758	CB	LYS	219	15.188	34.972	0.677	1.00	33.37
ATOM	1759	CG	LYS	219	14.707	35.722	1.911	1.00	34.09
ATOM	1760	CD	LYS	219	14.125	37.076	1.537	1.00	35.69
ATOM	1761	CE	LYS	219	13.682	37.852	2.765	1.00	39.13
ATOM	1762	NZ	LYS	219	13.047	39.158	2.399	1.00	40.00
ATOM	1763	C	LYS	219	14.745	34.118	-1.625	1.00	35.52
ATOM	1764	O	LYS	219	15.051	34.847	-2.573	1.00	34.96
ATOM	1765	N	LEU	220	14.950	32.807	-1.626	1.00	35.22
ATOM	1766	CA	LEU	220	15.566	32.138	-2.759	1.00	36.55
ATOM	1767	CB	LEU	220	15.877	30.690	-2.389	1.00	37.39
ATOM	1768	CG	LEU	220	16.647	29.830	-3.383	1.00	38.60
ATOM	1769	CD1	LEU	220	17.945	30.519	-3.792	1.00	38.29
ATOM	1770	CD2	LEU	220	16.936	28.489	-2.729	1.00	39.42
ATOM	1771	C	LEU	220	14.652	32.186	-3.979	1.00	37.19
ATOM	1772	O	LEU	220	15.102	32.465	-5.086	1.00	37.42
ATOM	1773	N	GLN	221	13.369	31.916	-3.773	1.00	38.14
ATOM	1774	CA	GLN	221	12.409	31.930	-4.870	1.00	39.61
ATOM	1775	CB	GLN	221	11.002	31.632	-4.350	1.00	43.16
ATOM	1776	CG	GLN	221	10.849	30.214	-3.829	1.00	47.61
ATOM	1777	CD	GLN	221	11.363	29.177	-4.820	1.00	51.15
ATOM	1778	OE1	GLN	221	10.772	28.966	-5.881	1.00	52.70
ATOM	1779	NE2	GLN	221	12.480	28.534	-4.479	1.00	51.82
ATOM	1780	C	GLN	221	12.420	33.261	-5.607	1.00	38.21
ATOM	1781	O	GLN	221	12.365	33.296	-6.835	1.00	37.75
ATOM	1782	N	VAL	222	12.497	34.354	-4.857	1.00	36.97
ATOM	1783	CA	VAL	222	12.529	35.676	-5.467	1.00	37.21
ATOM	1784	CB	VAL	222	12.377	36.795	-4.411	1.00	36.85
ATOM	1785	CG1	VAL	222	12.444	38.154	-5.086	1.00	37.24
ATOM	1786	CG2	VAL	222	11.050	36.645	-3.678	1.00	37.77
ATOM	1787	C	VAL	222	13.846	35.867	-6.217	1.00	37.47
ATOM	1788	O	VAL	222	13.869	36.424	-7.316	1.00	37.13
ATOM	1789	N	PHE	223	14.943	35.400	-5.624	1.00	37.83
ATOM	1790	CA	PHE	223	16.248	35.521	-6.268	1.00	39.20
ATOM	1791	CB	PHE	223	17.349	34.906	-5.392	1.00	37.95
ATOM	1792	CG	PHE	223	18.731	35.023	-5.984	1.00	39.28
ATOM	1793	CD1	PHE	223	19.405	36.238	-5.975	1.00	39.67
ATOM	1794	CD2	PHE	223	19.339	33.927	-6.589	1.00	39.69
ATOM	1795	CE1	PHE	223	20.666	36.362	-6.565	1.00	41.73
ATOM	1796	CE2	PHE	223	20.600	34.042	-7.180	1.00	40.32
ATOM	1797	CZ	PHE	223	21.262	35.263	-7.168	1.00	39.45
ATOM	1798	C	PHE	223	16.201	34.789	-7.612	1.00	40.64
ATOM	1799	O	PHE	223	16.767	35.249	-8.603	1.00	40.48
ATOM	1800	N	LYS	224	15.520	33.647	-7.634	1.00	42.33
ATOM	1801	CA	LYS	224	15.399	32.857	-8.851	1.00	45.23
ATOM	1802	CB	LYS	224	14.629	31.560	-8.571	1.00	47.13
ATOM	1803	CG	LYS	224	14.588	30.593	-9.749	1.00	50.45
ATOM	1804	CD	LYS	224	13.866	29.303	-9.383	1.00	52.28
ATOM	1805	CE	LYS	224	13.785	28.351	-10.572	1.00	54.02
ATOM	1806	NZ	LYS	224	13.051	27.088	-10.246	1.00	54.04
ATOM	1807	C	LYS	224	14.688	33.677	-9.925	1.00	45.85
ATOM	1808	O	LYS	224	14.990	33.545	-11.108	1.00	45.85
ATOM	1809	N	GLN	225	13.748	34.525	-9.509	1.00	47.18
ATOM	1810	CA	GLN	225	13.020	35.378	-10.448	1.00	48.45
ATOM	1811	CB	GLN	225	11.936	36.196	-9.732	1.00	49.96
ATOM	1812	CG	GLN	225	10.784	35.397	-9.136	1.00	51.68

ATOM	1813	CD	GLN	225	9.678	36.298	-8.600	1.00	53.23
ATOM	1814	OE1	GLN	225	9.911	37.141	-7.732	1.00	52.56
ATOM	1815	NE2	GLN	225	8.470	36.127	-9.123	1.00	53.37
ATOM	1816	C	GLN	225	13.990	36.352	-11.106	1.00	47.94
ATOM	1817	O	GLN	225	14.094	36.417	-12.331	1.00	48.26
ATOM	1818	N	SER	226	14.698	37.107	-10.272	1.00	48.06
ATOM	1819	CA	SER	226	15.658	38.104	-10.731	1.00	47.80
ATOM	1820	CB	SER	226	16.139	38.940	-9.542	1.00	47.91
ATOM	1821	OG	SER	226	15.055	39.594	-8.906	1.00	49.47
ATOM	1822	C	SER	226	16.871	37.533	-11.467	1.00	47.59
ATOM	1823	O	SER	226	17.314	38.099	-12.464	1.00	46.97
ATOM	1824	N	HIS	227	17.414	36.422	-10.979	1.00	47.93
ATOM	1825	CA	HIS	227	18.586	35.827	-11.614	1.00	47.70
ATOM	1826	CB	HIS	227	19.831	36.103	-10.769	1.00	48.42
ATOM	1827	CG	HIS	227	19.920	37.513	-10.273	1.00	48.29
ATOM	1828	CD2	HIS	227	20.711	38.543	-10.651	1.00	48.92
ATOM	1829	ND1	HIS	227	19.120	37.996	-9.260	1.00	48.46
ATOM	1830	CE1	HIS	227	19.418	39.263	-9.033	1.00	49.03
ATOM	1831	NE2	HIS	227	20.381	39.620	-9.864	1.00	50.21
ATOM	1832	C	HIS	227	18.439	34.324	-11.826	1.00	48.58
ATOM	1833	O	HIS	227	19.133	33.523	-11.189	1.00	47.32
ATOM	1834	N	PRO	228	17.543	33.921	-12.741	1.00	48.73
ATOM	1835	CD	PRO	228	16.807	34.782	-13.684	1.00	49.28
ATOM	1836	CA	PRO	228	17.303	32.504	-13.039	1.00	50.04
ATOM	1837	CB	PRO	228	16.245	32.563	-14.143	1.00	49.26
ATOM	1838	CG	PRO	228	16.574	33.846	-14.849	1.00	48.18
ATOM	1839	C	PRO	228	18.554	31.735	-13.471	1.00	50.55
ATOM	1840	O	PRO	228	18.823	30.641	-12.974	1.00	49.03
ATOM	1841	N	ASP	229	19.317	32.315	-14.392	1.00	51.87
ATOM	1842	CA	ASP	229	20.525	31.674	-14.901	1.00	53.58
ATOM	1843	CB	ASP	229	21.177	32.564	-15.964	1.00	55.87
ATOM	1844	CG	ASP	229	22.285	31.852	-16.723	1.00	58.49
ATOM	1845	OD1	ASP	229	22.014	30.790	-17.328	1.00	58.29
ATOM	1846	OD2	ASP	229	23.429	32.356	-16.719	1.00	61.04
ATOM	1847	C	ASP	229	21.543	31.343	-13.806	1.00	53.73
ATOM	1848	O	ASP	229	22.073	30.232	-13.765	1.00	53.65
ATOM	1849	N	ILE	230	21.817	32.304	-12.925	1.00	52.95
ATOM	1850	CA	ILE	230	22.776	32.094	-11.838	1.00	52.12
ATOM	1851	CB	ILE	230	22.850	33.326	-10.891	1.00	52.89
ATOM	1852	CG2	ILE	230	23.663	32.984	-9.644	1.00	51.95
ATOM	1853	CG1	ILE	230	23.479	34.520	-11.616	1.00	53.24
ATOM	1854	CD1	ILE	230	22.607	35.126	-12.699	1.00	55.39
ATOM	1855	C	ILE	230	22.405	30.868	-11.002	1.00	51.37
ATOM	1856	O	ILE	230	23.277	30.119	-10.553	1.00	50.26
ATOM	1857	N	VAL	231	21.105	30.672	-10.803	1.00	49.90
ATOM	1858	CA	VAL	231	20.601	29.554	-10.015	1.00	48.50
ATOM	1859	CB	VAL	231	19.103	29.753	-9.683	1.00	48.35
ATOM	1860	CG1	VAL	231	18.587	28.582	-8.857	1.00	47.45
ATOM	1861	CG2	VAL	231	18.908	31.063	-8.933	1.00	48.33
ATOM	1862	C	VAL	231	20.769	28.200	-10.701	1.00	48.45
ATOM	1863	O	VAL	231	21.269	27.245	-10.105	1.00	46.75
ATOM	1864	N	ASN	232	20.353	28.124	-11.959	1.00	48.93
ATOM	1865	CA	ASN	232	20.432	26.880	-12.708	1.00	49.80
ATOM	1866	CB	ASN	232	19.459	26.920	-13.889	1.00	53.19
ATOM	1867	CG	ASN	232	18.019	27.092	-13.448	1.00	56.24
ATOM	1868	OD1	ASN	232	17.513	26.322	-12.630	1.00	57.63
ATOM	1869	ND2	ASN	232	17.347	28.105	-13.991	1.00	57.88
ATOM	1870	C	ASN	232	21.816	26.527	-13.222	1.00	48.52
ATOM	1871	O	ASN	232	22.077	25.366	-13.534	1.00	48.20
ATOM	1872	N	THR	233	22.710	27.508	-13.300	1.00	47.20
ATOM	1873	CA	THR	233	24.042	27.241	-13.831	1.00	46.67
ATOM	1874	CB	THR	233	24.295	28.057	-15.122	1.00	46.77
ATOM	1875	OG1	THR	233	24.612	29.414	-14.787	1.00	47.29
ATOM	1876	CG2	THR	233	23.055	28.045	-16.001	1.00	46.89
ATOM	1877	C	THR	233	25.209	27.492	-12.887	1.00	45.74
ATOM	1878	O	THR	233	26.313	26.999	-13.121	1.00	46.15
ATOM	1879	N	LEU	234	24.987	28.256	-11.825	1.00	44.27
ATOM	1880	CA	LEU	234	26.078	28.536	-10.906	1.00	42.05
ATOM	1881	CB	LEU	234	26.278	30.049	-10.789	1.00	43.57
ATOM	1882	CG	LEU	234	26.870	30.673	-12.058	1.00	44.97
ATOM	1883	CD1	LEU	234	26.979	32.180	-11.909	1.00	46.57
ATOM	1884	CD2	LEU	234	28.240	30.068	-12.318	1.00	45.46
ATOM	1885	C	LEU	234	25.950	27.899	-9.523	1.00	40.08
ATOM	1886	O	LEU	234	26.941	27.410	-8.978	1.00	41.11
ATOM	1887	N	PHE	235	24.745	27.889	-8.960	1.00	36.54
ATOM	1888	CA	PHE	235	24.535	27.295	-7.637	1.00	33.39
ATOM	1889	CB	PHE	235	23.080	27.480	-7.190	1.00	33.46
ATOM	1890	CG	PHE	235	22.786	28.827	-6.591	1.00	31.78
ATOM	1891	CD1	PHE	235	23.700	29.867	-6.683	1.00	33.45
ATOM	1892	CD2	PHE	235	21.579	29.057	-5.942	1.00	33.88
ATOM	1893	CE1	PHE	235	23.416	31.120	-6.137	1.00	34.74

ATOM	1894	CE2	PHE	235	21.285	30.308	-5.393	1.00	33.31
ATOM	1895	CZ	PHE	235	22.205	31.338	-5.492	1.00	33.08
ATOM	1896	C	PHE	235	24.856	25.807	-7.651	1.00	30.87
ATOM	1897	O	PHE	235	24.744	25.154	-8.687	1.00	29.90
ATOM	1898	N	PRO	236	25.259	25.251	-6.498	1.00	29.01
ATOM	1899	CD	PRO	236	25.543	25.924	-5.220	1.00	27.51
ATOM	1900	CA	PRO	236	25.586	23.825	-6.408	1.00	28.71
ATOM	1901	CB	PRO	236	25.967	23.652	-4.941	1.00	27.24
ATOM	1902	CG	PRO	236	26.543	24.992	-4.598	1.00	28.61
ATOM	1903	C	PRO	236	24.372	22.985	-6.788	1.00	29.15
ATOM	1904	O	PRO	236	23.257	23.245	-6.336	1.00	27.23
ATOM	1905	N	PRO	237	24.573	21.966	-7.630	1.00	29.03
ATOM	1906	CD	PRO	237	25.811	21.603	-8.341	1.00	28.29
ATOM	1907	CA	PRO	237	23.460	21.113	-8.047	1.00	29.54
ATOM	1908	CB	PRO	237	24.166	19.971	-8.765	1.00	29.15
ATOM	1909	CG	PRO	237	25.285	20.697	-9.457	1.00	30.03
ATOM	1910	C	PRO	237	22.561	20.642	-6.898	1.00	30.20
ATOM	1911	O	PRO	237	21.334	20.703	-7.011	1.00	28.77
ATOM	1912	N	LEU	238	23.159	20.193	-5.795	1.00	29.38
ATOM	1913	CA	LEU	238	22.371	19.720	-4.652	1.00	29.57
ATOM	1914	CB	LEU	238	23.280	19.148	-3.558	1.00	28.08
ATOM	1915	CG	LEU	238	22.562	18.712	-2.271	1.00	27.84
ATOM	1916	CD1	LEU	238	21.542	17.633	-2.597	1.00	28.16
ATOM	1917	CD2	LEU	238	23.573	18.196	-1.250	1.00	25.13
ATOM	1918	C	LEU	238	21.504	20.828	-4.060	1.00	31.04
ATOM	1919	O	LEU	238	20.385	20.579	-3.608	1.00	31.07
ATOM	1920	N	TYR	239	22.022	22.051	-4.062	1.00	30.34
ATOM	1921	CA	TYR	239	21.290	23.189	-3.524	1.00	31.47
ATOM	1922	CB	TYR	239	22.196	24.419	-3.509	1.00	30.35
ATOM	1923	CG	TYR	239	21.607	25.640	-2.836	1.00	29.41
ATOM	1924	CD1	TYR	239	20.775	26.513	-3.535	1.00	30.76
ATOM	1925	CE1	TYR	239	20.284	27.672	-2.934	1.00	30.38
ATOM	1926	CD2	TYR	239	21.926	25.950	-1.514	1.00	28.97
ATOM	1927	CE2	TYR	239	21.442	27.101	-0.904	1.00	30.43
ATOM	1928	CZ	TYR	239	20.625	27.960	-1.624	1.00	30.74
ATOM	1929	OH	TYR	239	20.177	29.117	-1.037	1.00	35.16
ATOM	1930	C	TYR	239	20.056	23.442	-4.384	1.00	33.26
ATOM	1931	O	TYR	239	18.969	23.714	-3.870	1.00	32.84
ATOM	1932	N	LYS	240	20.223	23.348	-5.699	1.00	33.87
ATOM	1933	CA	LYS	240	19.100	23.546	-6.605	1.00	35.74
ATOM	1934	CB	LYS	240	19.580	23.506	-8.058	1.00	37.63
ATOM	1935	CG	LYS	240	18.468	23.659	-9.083	1.00	43.97
ATOM	1936	CD	LYS	240	19.026	23.682	-10.503	1.00	47.75
ATOM	1937	CE	LYS	240	17.906	23.676	-11.535	1.00	51.07
ATOM	1938	NZ	LYS	240	18.426	23.651	-12.941	1.00	52.39
ATOM	1939	C	LYS	240	18.059	22.447	-6.370	1.00	35.10
ATOM	1940	O	LYS	240	16.862	22.721	-6.270	1.00	35.12
ATOM	1941	N	GLU	241	18.529	21.209	-6.259	1.00	33.16
ATOM	1942	CA	GLU	241	17.657	20.060	-6.053	1.00	33.21
ATOM	1943	CB	GLU	241	18.483	18.767	-6.055	1.00	33.06
ATOM	1944	CG	GLU	241	17.684	17.505	-5.711	1.00	33.33
ATOM	1945	CD	GLU	241	18.533	16.243	-5.731	1.00	32.45
ATOM	1946	OE1	GLU	241	19.105	15.919	-6.792	1.00	35.20
ATOM	1947	OE2	GLU	241	18.629	15.569	-4.687	1.00	33.93
ATOM	1948	C	GLU	241	16.832	20.125	-4.776	1.00	33.04
ATOM	1949	O	GLU	241	15.664	19.747	-4.771	1.00	34.27
ATOM	1950	N	LEU	242	17.434	20.607	-3.695	1.00	33.22
ATOM	1951	CA	LEU	242	16.740	20.682	-2.416	1.00	34.25
ATOM	1952	CB	LEU	242	17.754	20.729	-1.271	1.00	32.75
ATOM	1953	CG	LEU	242	18.705	19.539	-1.138	1.00	34.23
ATOM	1954	CD1	LEU	242	19.752	19.841	-0.083	1.00	35.05
ATOM	1955	CD2	LEU	242	17.926	18.292	-0.779	1.00	35.31
ATOM	1956	C	LEU	242	15.782	21.853	-2.256	1.00	35.37
ATOM	1957	O	LEU	242	14.755	21.721	-1.597	1.00	34.72
ATOM	1958	N	PHE	243	16.113	22.992	-2.854	1.00	37.53
ATOM	1959	CA	PHE	243	15.286	24.182	-2.710	1.00	41.05
ATOM	1960	CB	PHE	243	16.129	25.297	-2.090	1.00	38.64
ATOM	1961	CG	PHE	243	16.939	24.850	-0.897	1.00	37.15
ATOM	1962	CD1	PHE	243	18.329	24.797	-0.962	1.00	34.33
ATOM	1963	CD2	PHE	243	16.309	24.446	0.277	1.00	34.27
ATOM	1964	CE1	PHE	243	19.082	24.346	0.123	1.00	34.36
ATOM	1965	CE2	PHE	243	17.051	23.992	1.369	1.00	36.44
ATOM	1966	CZ	PHE	243	18.442	23.941	1.291	1.00	34.07
ATOM	1967	C	PHE	243	14.594	24.690	-3.975	1.00	45.43
ATOM	1968	O	PHE	243	14.154	25.842	-4.021	1.00	45.60
ATOM	1969	N	ASN	244	14.496	23.835	-4.992	1.00	50.27
ATOM	1970	CA	ASN	244	13.827	24.187	-6.248	1.00	54.32
ATOM	1971	CB	ASN	244	14.845	24.575	-7.327	1.00	55.30
ATOM	1972	CG	ASN	244	15.432	25.954	-7.105	1.00	58.57
ATOM	1973	OD1	ASN	244	14.720	26.961	-7.151	1.00	59.86
ATOM	1974	ND2	ASN	244	16.737	26.010	-6.861	1.00	60.33

ATOM	1975	C	ASN	244	12.977	23.028	-6.749	1.00	55.97
ATOM	1976	O	ASN	244	11.823	23.215	-7.137	1.00	58.40
ATOM	1977	N	HIS	691	15.075	13.032	-6.848	1.00	41.98
ATOM	1978	CA	HIS	691	16.238	13.605	-6.167	1.00	42.61
ATOM	1979	CB	HIS	691	15.999	13.671	-4.658	1.00	45.30
ATOM	1980	CG	HIS	691	14.679	14.268	-4.285	1.00	47.14
ATOM	1981	CD2	HIS	691	14.328	15.542	-3.992	1.00	47.32
ATOM	1982	ND1	HIS	691	13.518	13.527	-4.227	1.00	48.40
ATOM	1983	CE1	HIS	691	12.509	14.318	-3.913	1.00	49.67
ATOM	1984	NE2	HIS	691	12.973	15.547	-3.765	1.00	50.69
ATOM	1985	C	HIS	691	17.466	12.756	-6.442	1.00	41.10
ATOM	1986	O	HIS	691	17.940	12.027	-5.570	1.00	39.31
ATOM	1987	N	LYS	692	17.977	12.862	-7.661	1.00	40.46
ATOM	1988	CA	LYS	692	19.136	12.092	-8.079	1.00	40.37
ATOM	1989	CB	LYS	692	19.497	12.451	-9.523	1.00	42.93
ATOM	1990	CG	LYS	692	20.567	11.554	-10.137	1.00	47.97
ATOM	1991	CD	LYS	692	20.901	11.967	-11.569	1.00	51.10
ATOM	1992	CE	LYS	692	21.771	10.913	-12.257	1.00	52.83
ATOM	1993	NZ	LYS	692	23.026	10.630	-11.497	1.00	54.26
ATOM	1994	C	LYS	692	20.354	12.299	-7.177	1.00	38.35
ATOM	1995	O	LYS	692	20.951	11.336	-6.697	1.00	37.83
ATOM	1996	N	ILE	693	20.714	13.553	-6.941	1.00	35.38
ATOM	1997	CA	ILE	693	21.882	13.854	-6.122	1.00	35.12
ATOM	1998	CB	ILE	693	22.166	15.363	-6.123	1.00	32.22
ATOM	1999	CG2	ILE	693	23.426	15.656	-5.328	1.00	33.60
ATOM	2000	CG1	ILE	693	22.336	15.844	-7.568	1.00	34.55
ATOM	2001	CD1	ILE	693	22.439	17.342	-7.716	1.00	32.01
ATOM	2002	C	ILE	693	21.788	13.355	-4.678	1.00	33.70
ATOM	2003	O	ILE	693	22.664	12.636	-4.205	1.00	31.97
ATOM	2004	N	LEU	694	20.730	13.742	-3.978	1.00	33.87
ATOM	2005	CA	LEU	694	20.560	13.328	-2.592	1.00	35.23
ATOM	2006	CB	LEU	694	19.232	13.866	-2.050	1.00	36.03
ATOM	2007	CG	LEU	694	18.964	13.754	-0.549	1.00	36.23
ATOM	2008	CD1	LEU	694	20.078	14.436	0.243	1.00	33.63
ATOM	2009	CD2	LEU	694	17.622	14.395	-0.241	1.00	34.69
ATOM	2010	C	LEU	694	20.587	11.804	-2.520	1.00	35.61
ATOM	2011	O	LEU	694	21.159	11.212	-1.602	1.00	33.23
ATOM	2012	N	HIS	695	19.982	11.178	-3.520	1.00	36.63
ATOM	2013	CA	HIS	695	19.913	9.729	-3.595	1.00	39.34
ATOM	2014	CB	HIS	695	19.071	9.324	-4.805	1.00	43.87
ATOM	2015	CG	HIS	695	18.316	8.049	-4.616	1.00	50.18
ATOM	2016	CD2	HIS	695	16.985	7.800	-4.582	1.00	51.51
ATOM	2017	ND1	HIS	695	18.939	6.831	-4.437	1.00	52.83
ATOM	2018	CE1	HIS	695	18.024	5.887	-4.305	1.00	52.75
ATOM	2019	NE2	HIS	695	16.830	6.448	-4.389	1.00	53.18
ATOM	2020	C	HIS	695	21.317	9.153	-3.717	1.00	39.12
ATOM	2021	O	HIS	695	21.658	8.158	-3.068	1.00	40.09
ATOM	2022	N	ARG	696	22.139	9.784	-4.545	1.00	37.19
ATOM	2023	CA	ARG	696	23.496	9.307	-4.730	1.00	36.26
ATOM	2024	CB	ARG	696	24.199	10.085	-5.835	1.00	37.76
ATOM	2025	CG	ARG	696	25.596	9.562	-6.085	1.00	39.24
ATOM	2026	CD	ARG	696	26.427	10.510	-6.899	1.00	40.46
ATOM	2027	NE	ARG	696	27.767	9.968	-7.097	1.00	43.23
ATOM	2028	CZ	ARG	696	28.741	10.610	-7.730	1.00	44.16
ATOM	2029	NH1	ARG	696	28.520	11.823	-8.221	1.00	42.50
ATOM	2030	NH2	ARG	696	29.927	10.033	-7.884	1.00	43.92
ATOM	2031	C	ARG	696	24.308	9.431	-3.447	1.00	34.63
ATOM	2032	O	ARG	696	25.043	8.517	-3.081	1.00	32.87
ATOM	2033	N	LEU	697	24.174	10.567	-2.769	1.00	32.92
ATOM	2034	CA	LEU	697	24.918	10.800	-1.538	1.00	32.40
ATOM	2035	CB	LEU	697	24.693	12.235	-1.047	1.00	29.94
ATOM	2036	CG	LEU	697	25.210	13.332	-1.989	1.00	28.77
ATOM	2037	CD1	LEU	697	24.983	14.716	-1.377	1.00	27.97
ATOM	2038	CD2	LEU	697	26.686	13.116	-2.257	1.00	28.17
ATOM	2039	C	LEU	697	24.567	9.793	-0.446	1.00	33.91
ATOM	2040	O	LEU	697	25.447	9.321	0.282	1.00	33.09
ATOM	2041	N	LEU	698	23.287	9.455	-0.338	1.00	35.43
ATOM	2042	CA	LEU	698	22.836	8.494	0.662	1.00	39.05
ATOM	2043	CB	LEU	698	21.317	8.332	0.605	1.00	36.77
ATOM	2044	CG	LEU	698	20.470	9.189	1.534	1.00	35.45
ATOM	2045	CD1	LEU	698	19.002	8.875	1.295	1.00	33.66
ATOM	2046	CD2	LEU	698	20.857	8.902	2.977	1.00	34.33
ATOM	2047	C	LEU	698	23.464	7.119	0.473	1.00	41.14
ATOM	2048	O	LEU	698	23.649	6.374	1.434	1.00	41.09
ATOM	2049	N	GLN	699	23.790	6.786	-0.769	1.00	44.86
ATOM	2050	CA	GLN	699	24.355	5.478	-1.064	1.00	48.97
ATOM	2051	CB	GLN	699	23.629	4.895	-2.278	1.00	50.91
ATOM	2052	CG	GLN	699	22.142	5.248	-2.281	1.00	54.28
ATOM	2053	CD	GLN	699	21.316	4.356	-3.180	1.00	56.50
ATOM	2054	OE1	GLN	699	21.080	3.187	-2.866	1.00	57.96
ATOM	2055	NE2	GLN	699	20.870	4.901	-4.309	1.00	57.46

ATOM	2056	C	GLN	699	25.866	5.479	-1.285	1.00	49.73
ATOM	2057	O	GLN	699	26.471	4.426	-1.486	1.00	50.77
ATOM	2058	N	GLU	700	26.475	6.658	-1.237	1.00	50.70
ATOM	2059	CA	GLU	700	27.917	6.773	-1.426	1.00	51.84
ATOM	2060	CB	GLU	700	28.326	8.248	-1.470	1.00	52.07
ATOM	2061	CG	GLU	700	29.708	8.509	-2.060	1.00	53.82
ATOM	2062	CD	GLU	700	29.815	8.077	-3.516	1.00	53.97
ATOM	2063	OE1	GLU	700	28.904	8.404	-4.307	1.00	54.46
ATOM	2064	OE2	GLU	700	30.815	7.419	-3.871	1.00	55.26
ATOM	2065	C	GLU	700	28.627	6.070	-0.269	1.00	52.20
ATOM	2066	O	GLU	700	29.459	5.175	-0.527	1.00	52.35
ATOM	2067	OXT	GLU	700	28.335	6.428	0.891	1.00	52.40
ATOM	2068	OH2	WAT	801	14.711	26.653	2.728	1.00	24.40
ATOM	2069	OH2	WAT	802	26.414	20.512	8.977	1.00	20.53
ATOM	2070	OH2	WAT	803	25.635	40.975	13.967	1.00	28.74
ATOM	2071	OH2	WAT	804	13.552	16.269	8.746	1.00	21.45
ATOM	2072	OH2	WAT	805	21.059	40.743	3.993	1.00	34.61
ATOM	2073	OH2	WAT	806	11.847	19.482	13.154	1.00	27.86
ATOM	2074	OH2	WAT	807	24.620	17.326	14.726	1.00	20.00
ATOM	2075	OH2	WAT	808	25.763	19.395	-5.509	1.00	24.65
ATOM	2076	OH2	WAT	809	27.566	41.817	2.053	1.00	34.09
ATOM	2077	OH2	WAT	810	1.729	8.907	4.075	1.00	31.53
ATOM	2078	OH2	WAT	811	7.205	27.241	11.662	1.00	35.98
ATOM	2079	OH2	WAT	812	23.647	26.541	23.470	1.00	28.06
ATOM	2080	OH2	WAT	813	14.409	33.457	14.799	1.00	33.72
ATOM	2081	OH2	WAT	814	13.065	3.124	16.758	1.00	28.22
ATOM	2082	OH2	WAT	815	30.885	19.043	2.598	1.00	33.40
ATOM	2083	OH2	WAT	816	36.157	39.234	1.950	1.00	43.36
ATOM	2084	OH2	WAT	817	12.139	22.822	7.031	1.00	30.28
ATOM	2085	OH2	WAT	818	3.298	4.825	10.176	1.00	23.53
ATOM	2086	OH2	WAT	819	1.704	13.633	4.812	1.00	22.44
ATOM	2087	OH2	WAT	820	4.214	13.018	8.864	1.00	29.86
ATOM	2088	OH2	WAT	821	0.762	10.736	7.722	1.00	36.08
ATOM	2089	OH2	WAT	822	0.166	11.985	3.762	1.00	37.47
ATOM	2090	OH2	WAT	823	31.803	41.991	11.509	1.00	38.01
ATOM	2091	OH2	WAT	825	29.323	24.136	13.813	1.00	31.41
ATOM	2092	OH2	WAT	832	15.159	19.303	30.516	1.00	39.31
ATOM	2093	OH2	WAT	835	3.146	11.579	6.786	1.00	34.28
ATOM	2094	OH2	WAT	836	8.412	22.351	12.154	1.00	37.30
ATOM	2095	OH2	WAT	837	14.427	24.078	4.226	1.00	33.47
ATOM	2096	OH2	WAT	839	2.395	4.154	7.605	1.00	29.06
ATOM	2097	OH2	WAT	840	26.537	16.496	27.832	1.00	31.09
ATOM	2098	OH2	WAT	841	8.106	20.585	7.958	1.00	33.63
ATOM	2099	OH2	WAT	842	11.326	3.463	14.716	1.00	31.28
ATOM	2100	OH2	WAT	843	14.267	3.376	12.820	1.00	30.09
ATOM	2101	OH2	WAT	844	12.746	22.210	13.480	1.00	53.73
ATOM	2102	OH2	WAT	846	34.204	40.570	11.521	1.00	54.26
ATOM	2103	OH2	WAT	847	9.625	5.990	8.120	1.00	29.28
ATOM	2104	OH2	WAT	848	9.201	31.722	7.032	1.00	45.91
ATOM	2105	OH2	WAT	849	12.004	24.958	5.330	1.00	32.20
ATOM	2106	OH2	WAT	850	37.886	45.476	1.031	1.00	31.54
ATOM	2107	OH2	WAT	851	31.059	28.266	8.430	1.00	44.76
ATOM	2108	OH2	WAT	852	19.435	16.697	-9.090	1.00	46.89
ATOM	2109	OH2	WAT	853	18.131	44.059	3.829	1.00	54.92
ATOM	2110	OH2	WAT	854	26.481	10.672	28.939	1.00	48.07
ATOM	2111	OH2	WAT	855	6.654	19.232	5.941	1.00	41.68
ATOM	2112	OH2	WAT	856	9.668	17.943	18.268	1.00	32.85
ATOM	2113	OH2	WAT	857	10.512	10.846	24.734	1.00	38.33
ATOM	2114	OH2	WAT	858	20.864	44.415	2.676	1.00	50.37
ATOM	2115	OH2	WAT	859	10.258	-0.353	5.697	1.00	56.40
ATOM	2116	OH2	WAT	860	2.560	9.064	21.518	1.00	69.57
ATOM	2117	OH2	WAT	861	33.537	17.935	17.817	1.00	38.63
ATOM	2118	OH2	WAT	862	7.370	24.146	6.448	1.00	36.09
ATOM	2119	OH2	WAT	863	30.158	20.333	25.058	1.00	30.28
ATOM	2120	OH2	WAT	865	30.909	40.546	-7.045	1.00	44.78
ATOM	2121	OH2	WAT	866	15.610	43.031	8.646	1.00	47.88
ATOM	2122	OH2	WAT	867	12.882	25.860	0.818	1.00	36.53
ATOM	2123	OH2	WAT	868	36.979	45.229	-7.650	1.00	75.27
ATOM	2124	OH2	WAT	869	9.261	19.297	12.679	1.00	36.84
ATOM	2125	OH2	WAT	870	15.360	22.134	6.145	1.00	36.08
ATOM	2126	OH2	WAT	871	23.204	42.943	6.553	1.00	55.50
ATOM	2127	OH2	WAT	873	24.254	39.737	21.553	1.00	69.04
ATOM	2128	OH2	WAT	874	20.154	35.236	-14.461	1.00	40.58
ATOM	2129	OH2	WAT	875	5.710	19.528	10.717	1.00	51.87
ATOM	2130	OH2	WAT	876	22.924	24.573	-10.275	1.00	59.21
ATOM	2131	OH2	WAT	877	12.716	26.906	-1.662	1.00	46.87
ATOM	2132	OH2	WAT	878	29.438	8.222	21.664	1.00	31.21
ATOM	2133	OH2	WAT	879	20.109	5.113	16.032	1.00	39.95
ATOM	2134	OH2	WAT	880	24.412	46.283	17.227	1.00	55.64
ATOM	2135	OH2	WAT	881	28.720	9.423	6.651	1.00	32.54
ATOM	2136	OH2	WAT	883	42.162	41.811	5.003	1.00	55.81

ATOM	2137	OH2	WAT	884	7.066	29.019	8.902	1.00	52.17
ATOM	2138	OH2	WAT	885	18.047	2.153	2.538	1.00	50.39
ATOM	2139	OH2	WAT	886	24.362	3.892	9.915	1.00	41.25
ATOM	2140	OH2	WAT	887	15.604	37.471	-2.711	1.00	42.93
ATOM	2141	OH2	WAT	889	4.907	3.035	10.619	1.00	41.58
ATOM	2142	OH2	WAT	890	21.088	8.951	-7.950	1.00	37.07
ATOM	2143	OH2	WAT	891	26.883	7.714	24.992	1.00	38.03
ATOM	2144	OH2	WAT	892	27.672	6.863	14.497	1.00	33.97
ATOM	2145	OH2	WAT	893	32.830	16.371	13.351	1.00	39.04
ATOM	2146	OH2	WAT	894	27.935	24.454	28.849	1.00	58.27
ATOM	2147	OH2	WAT	895	31.271	29.479	18.350	1.00	35.40
ATOM	2148	OH2	WAT	896	20.663	0.959	10.098	1.00	29.75
ATOM	2149	OH2	WAT	898	25.086	4.474	5.856	1.00	58.91
ATOM	2150	OH2	WAT	899	10.823	19.991	1.639	1.00	50.34
ATOM	2151	OH2	WAT	900	36.503	19.016	22.377	1.00	47.47
ATOM	2152	OH2	WAT	901	7.753	18.823	14.805	1.00	63.11
ATOM	2153	OH2	WAT	902	39.898	36.941	0.917	1.00	58.76
ATOM	2154	OH2	WAT	903	9.902	17.486	15.681	1.00	43.86
ATOM	2155	OH2	WAT	904	10.082	39.246	11.235	1.00	61.89
ATOM	2156	OH2	WAT	905	11.163	31.359	-8.260	1.00	56.41
ATOM	2157	OH2	WAT	906	31.409	30.077	0.054	1.00	38.17
ATOM	2158	OH2	WAT	907	-0.262	4.591	11.602	1.00	40.33
ATOM	2159	OH2	WAT	908	31.641	28.926	2.593	1.00	66.15
ATOM	2160	OH2	WAT	909	-1.843	16.272	8.893	1.00	44.52
ATOM	2161	OH2	WAT	910	10.182	38.951	7.471	1.00	67.08
ATOM	2162	OH2	WAT	911	13.297	1.372	1.110	1.00	53.70
ATOM	2163	OH2	WAT	912	15.299	2.429	15.304	1.00	39.81
ATOM	2164	OH2	WAT	913	16.202	17.257	31.878	1.00	39.68
ATOM	2165	OH2	WAT	914	33.600	36.849	17.451	1.00	35.02
ATOM	2166	OH2	WAT	915	-0.283	12.217	10.059	1.00	33.29
ATOM	2167	OH2	WAT	916	20.496	1.221	17.973	1.00	45.64
ATOM	2168	OH2	WAT	917	22.207	39.746	15.987	1.00	51.55
ATOM	2169	OH2	WAT	918	14.385	33.613	17.595	1.00	42.92
ATOM	2170	OH2	WAT	919	26.248	13.606	-7.378	1.00	37.16
ATOM	2171	OH2	WAT	920	25.959	6.408	-4.445	1.00	48.88
ATOM	2172	OH2	WAT	921	17.591	2.898	16.434	1.00	39.25
ATOM	2173	OH2	WAT	922	33.239	45.203	11.047	1.00	49.84
ATOM	2174	OH2	WAT	923	12.608	31.888	-12.406	1.00	50.03
ATOM	2175	OH2	WAT	924	26.381	45.820	0.731	1.00	44.95
ATOM	2176	OH2	WAT	925	7.350	22.130	18.821	1.00	48.55
ATOM	2177	OH2	WAT	926	23.505	34.031	25.189	1.00	52.64
ATOM	2178	OH2	WAT	927	23.404	53.128	-2.298	1.00	76.10
ATOM	2179	OH2	WAT	928	29.823	49.147	1.695	1.00	48.44
ATOM	2180	OH2	WAT	929	21.489	3.727	1.417	1.00	61.20
ATOM	2181	OH2	WAT	930	18.898	35.011	-16.838	1.00	67.70
ATOM	2182	OH2	WAT	931	8.048	22.678	24.638	1.00	35.53
ATOM	2183	OH2	WAT	933	33.982	42.818	-3.037	1.00	40.39
ATOM	2184	OH2	WAT	934	9.979	28.055	25.701	1.00	46.53
ATOM	2185	OH2	WAT	935	13.628	22.137	2.420	1.00	44.85
ATOM	2186	OH2	WAT	936	19.171	1.332	15.385	1.00	37.36
ATOM	2187	OH2	WAT	939	27.207	28.433	-6.434	1.00	68.57
ATOM	2188	OH2	WAT	940	3.857	1.418	8.795	1.00	68.25
ATOM	2189	OH2	WAT	941	16.520	42.036	-2.158	1.00	79.07
ATOM	2190	OH2	WAT	942	17.605	46.558	2.927	1.00	47.55
ATOM	2191	OH2	WAT	943	15.096	42.405	3.989	1.00	53.50
ATOM	2192	OH2	WAT	950	9.314	22.415	6.528	1.00	40.77
ATOM	2193	OH2	WAT	951	5.922	25.754	4.200	1.00	58.05
ATOM	2194	OH2	WAT	952	-0.116	13.000	6.780	1.00	96.22
ATOM	2195	OH2	WAT	954	33.641	28.462	7.707	1.00	38.33
ATOM	2196	OH2	WAT	955	20.020	19.781	-9.186	1.00	46.18
ATOM	2197	OH2	WAT	956	22.350	22.390	-11.831	1.00	44.39
ATOM	2198	C1	REA	500	22.676	32.386	7.585	1.00	44.19
ATOM	2199	C2	REA	500	21.906	33.574	6.875	1.00	44.67
ATOM	2200	C3	REA	500	21.637	33.455	5.374	1.00	44.62
ATOM	2201	C4	REA	500	22.790	32.926	4.506	1.00	44.15
ATOM	2202	C5	REA	500	23.891	32.096	5.255	1.00	43.36
ATOM	2203	C6	REA	500	23.862	31.835	6.638	1.00	42.89
ATOM	2204	C7	REA	500	24.919	31.045	7.334	1.00	41.43
ATOM	2205	C8	REA	500	25.046	29.710	7.573	1.00	38.85
ATOM	2206	C9	REA	500	26.080	29.094	8.397	1.00	39.63
ATOM	2207	C10	REA	500	26.066	27.725	8.531	1.00	37.78
ATOM	2208	C11	REA	500	27.051	27.018	9.329	1.00	37.42
ATOM	2209	C12	REA	500	27.070	25.694	9.440	1.00	37.89
ATOM	2210	C13	REA	500	28.057	24.977	10.242	1.00	38.53
ATOM	2211	C14	REA	500	27.951	23.626	10.224	1.00	36.87
ATOM	2212	C15	REA	500	28.705	22.564	10.870	1.00	35.41
ATOM	2213	C16	REA	500	21.650	31.254	7.888	1.00	44.23
ATOM	2214	C17	REA	500	23.235	32.990	8.910	1.00	45.49
ATOM	2215	C18	REA	500	24.948	31.651	4.234	1.00	43.96
ATOM	2216	C19	REA	500	27.157	29.991	9.084	1.00	37.79
ATOM	2217	C20	REA	500	29.159	25.776	11.043	1.00	39.49

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ATOM   2218  O1  REA   500      28.377  21.424  10.626  1.00 36.24
ATOM   2219  O2  REA   500      29.641  22.779  11.628  1.00 31.52
END
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CLAIMS

1. Polypeptides derived from the retinoic acid-related orphan receptor (ROR) in mammals, characterized in that they are delimited in their N-terminal extremity by an amino-acid located between positions 1 to 209 of the rat, human, or murine RORβ, α, or γ, as represented on figure 3, or by an amino-acid located at corresponding positions in nuclear receptor ROR of other subtypes than α, β and γ, and/or of other mammals, and in their C-terminal extremity by an amino-acid located between positions 450 to 452 of the rat, human, or murine RORβ, α, or γ, as represented on figure 3, or by an amino-acid located at corresponding positions in nuclear receptor ROR of other subtypes than α, β and γ, and/or of other mammals.

2. Polypeptides according to claim 1, characterized in that at least the approximately 100 to 200 first amino-acids of the N-terminal part of the sequence of said receptor is deleted.

3. Polypeptides according to claim 1 or 2, derived from the nuclear receptor ROR, wherein the binding properties of the ligand-binding domain, or LBD, of said receptor, are maintained.

4. Polypeptides derived from the nuclear receptor RORβ, of mammals, such as human or rat, these derived polypeptides comprising a polypeptide as defined in claims 1 to 3, such as the polypeptides delimited by the amino-acids located in positions 201 to 459 of the sequences of rat or human RORβ represented on figure 3, said polypeptides being characterized in that at least one of the cysteine in position 454 or in position 458 of the amino-acid sequence of said nuclear receptor RORβ, as represented on figure 3, is deleted or substituted by another amino-acid, natural or not, such as alanine or serine.

5. Polypeptides according to any of claims 1 to 3, characterized in that they correspond to the fragments of mammals ROR, and more particularly of rat, human, or murine RORβ, α, or γ, delimited in their N-terminal extremity by the amino acid located in one of the positions 201 to 209 of the ROR sequences represented on figure 3, and in their C-terminal extremity by the amino acid located in one of the positions 451 or 452, of the ROR sequences represented on figure 3.

6. Polypeptides according to any of claims 1 to 5, as defined above, chosen among :
- the fragment delimited by the amino acids located in positions 209 to 452 of :
  . the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 2,
  . the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 3,
  . the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 4,
  . the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 5,
  . the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 6,
  . the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 7,
- the fragment delimited by the amino acids located in positions 208 to 452 of :
  . the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 8,
  . the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 9,
  . the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 10,

. the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 11,
. the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 12,
. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 13,
- the fragment delimited by the amino acids located in positions 208 to 451 of :
. the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 14,
. the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 15,
. the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 16,
. the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 17,
. the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 18,
. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 19,
- the fragment delimited by the amino acids located in positions 209 to 451 of :
. the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 20,
. the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 21,
. the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 22,
. the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 23,
. the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 24,
. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 25,
- the fragment delimited by the amino acids located in positions 201 to 451 of :
. the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 26,
. the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 27,
. the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 28,
. the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 29,
. the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 30,
. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 31,
- the fragment delimited by the amino acids located in positions 201 to 452 of :
. the sequence of the rat RORβ represented on figure 3, and corresponding to SEQ ID NO : 32,
. the sequence of the human RORβ represented on figure 3, and corresponding to SEQ ID NO : 33,
. the sequence of the human RORγ represented on figure 3, and corresponding to SEQ ID NO : 34,
. the sequence of the murine RORγ represented on figure 3, and corresponding to SEQ ID NO : 35,
. the sequence of the human RORα represented on figure 3, and corresponding to SEQ ID NO : 36,

. the sequence of the murine RORα represented on figure 3, and corresponding to SEQ ID NO : 37.

7. Polypeptides according to any one of claims 1 to 6, characterized by the following characteristics :
- they have the properties of binding a ligand and of transactivation of the LBD of the receptor ROR,
- they are soluble in aqueous solvants,
- they are crystallisable in aqueous solvents, especially by the hanging drop vapour diffusion method, more particularly at approximately 4°C

or polypeptides or peptide sequences derived of those above mentioned, for example by suppression, addition or substitution of one or several amino acids, these polypeptides or peptide sequences having the characterisitics above mentioned.

8. Molecular complexes comprising a polypeptide according to any one of claims 1 to 7, said polypeptide being in association with :
- a ROR-LBD ligand which is an agonist, such as stearic acid, or an antagonist of the ROR-LBD, such as retinoic acid,
- and/or with a co-peptide having a sequence of approximately 15-20 amino-acids and comprising the co-activator motif LXXLL or a co-repressor motif (I/L)XX(V/I)I or LXX(H/I)IXXX(I/L) wherein X represents any amino acid, natural or not, such as co-peptides chosen among fragments of co-activators of transcription, especially those of the p160 family, and more particularly among fragments of the co-activators SRC1, such as the fragment 686-700 of SRC1, or among fragments of co-repressors of transcription.

9. Nucleotide sequence coding for a polypeptide according to any one of claims 1 to 7.

10. Nucleotide sequence according to claim 9, associated to elements necessary for the transcription of this sequence, particularly a promoter and a terminator of transcription.

11. Vector, particularly plasmid, comprising a nucleotide sequence according to claim 9 or 11.

12. Host cells, such as *E.coli*, transformed with a vector according to claim 11.

13. Process for obtaining a polypeptide according to any one of claims 1 to 7, or a molecular complex according to claim 10, characterized in that it comprises :
- a step of transforming host cells with a nucleotide sequence according to claim 9 or 10, using a vector according to claim 11,
- a step of cultivating the transformed host cell according to claim 12 thus obtained, in an appropriate culture medium,
- and the recovery, and if necessary, the purification of the recombinant polypeptide or molecular complex obtained.

14. A crystal comprising a polypeptide according to any one of claims 1 to 9, or a molecular complex according to claim 10.

15. A crystal according to claim 14, characterized in that said crystal diffracts to at least 3 angstrom resolution and has a crystal stability within 5% of its unit cell dimensions.

16. A crystal according to claim 14 or 15, wherein the ROR-LBD has the following unit cell dimensions in angstroms : a= 52.302 Å, b= 58.490 Å and c= 106.036 Å, $\alpha=\beta=\chi=90$ °, and an orthorhombic space group P212121.

17. A crystal according to any one of claims 14 to 16, such as obtained by carrying out a process according to claim 13, and comprising a step of crystallisation in aqueous solvents of the polypeptides any one of claims 1 to 7, or the molecular complexes according to claim 8, especially at 4°C by the hanging drop vapour diffusion method,

18. Use of the polypeptides according to any one of claims 1 to 7, or of the molecular complexes according to claim 10, or of the crystals according to any one of claims 14 to 17, for carrying out :

- a process for the screening of a ROR-LBD ligand which is an agonist, or an antagonist of said receptor, or for the screening of ligands that perturb the structure of the receptor and having an effect on the recruitment of cofactors (co-activators and co-repressors) and hence on gene regulation,
- or a process for the analysis of the tridimensional structure of the complexes formed with said polypeptides, molecular complexes or crystals and a particular compound.

19. Use according to claim 18, for the screening of compounds acting as agonists or antagonists of ROR, said compounds being useful in the frame of the treatment of pathologies related to the central nervous system, the retinal organisation, the sensorial signal integration, the motricity, and sterility.

20. Process for the screening of a ROR-LBD ligand which is an agonist, or an antagonist of said receptor, said process comprising the following steps :

- contacting a polypeptide according to any one of claims 1 to 7, or a molecular complex according to claim 8, or a crystal according to any one of claims 14 to 17, advantageously linked to a solid support, with the particular compound susceptible to be a ROR-LBD ligand, preferably one of the said polypeptide, or molecular complex, or crystal, or tested ligand, being labelled, such as with a fluorescent, radioactive or enzymatic label,
- detection of the possible association between the said polypeptide, or molecular complex, or crystal, and the tested ligand, by measuring the used label, especially after rinsing the support used in the preceding step, or by mass spectrometry under non denaturing conditions.

21. Process for the analysis of the tridimensional structure of the complexes formed with a polypeptide according to any one of claims 1 to 7, or a molecular complex according to claim 8, or a crystal according to any one of claims 14 to 17, and a particular compound susceptible to be a ROR-LBD ligand, said process comprising the following steps :

- contacting the said polypeptide, or molecular complex, or crystal, with said particular compound,
- crystallisation of the complex formed between the said polypeptide, or molecular complex, or crystal, and the tested ligand, especially with the vapour diffusion method, and tridimensional analysis of said complex, especially with the molecular replacement method,
- or tridimensional analysis of said complex in soluble state, by using an appropriate method such as NMR.

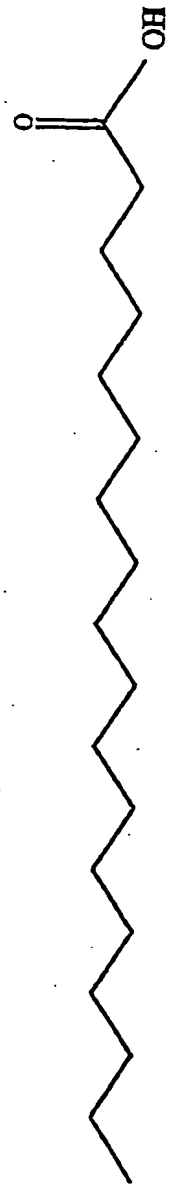

Figure 1

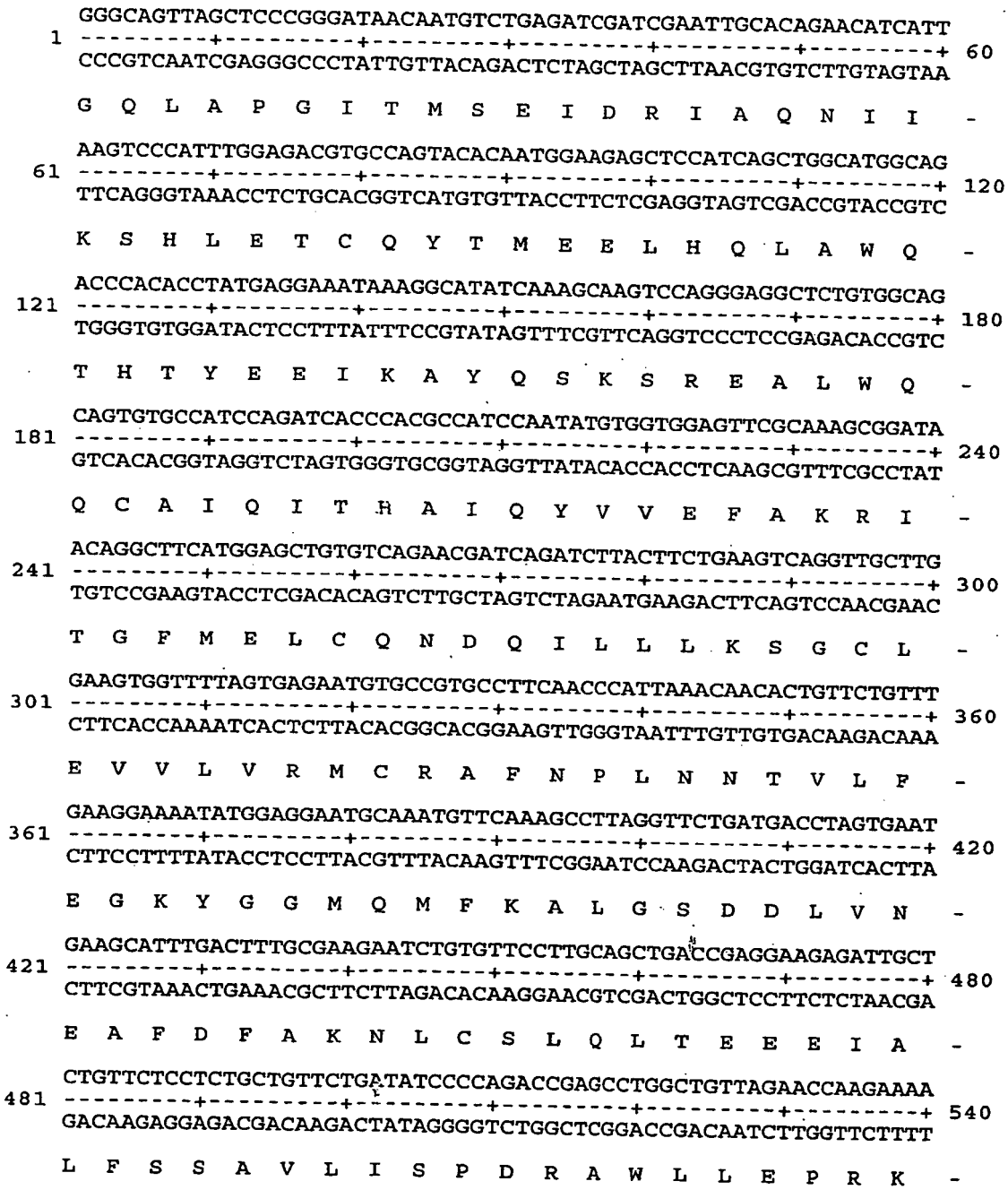

FIGURE 2

```
    GTCCAGAAGCTTCAGGAAAAAATTTATTTTGCACTTCAACATGTGATTCAGAAGAATCAC
541 ---------+---------+---------+---------+---------+---------+ 600
    CAGGTCTTCGAAGTCCTTTTTTAAATAAAACGTGAAGTTGTACACTAAGTCTTCTTAGTG

    V  Q  K  L  Q  E  K  I  Y  F  A  L  Q  H  V  I  Q  K  N  H  -

    CTGGATGATGAGACCCTGGCAAAGTTAATAGCCAAGATACCAACTATCACGGCAGTCTGC
601 ---------+---------+---------+---------+---------+---------+ 660
    GACCTACTACTCTGGGACCGTTTCAATTATCGGTTCTATGGTTGATAGTGCCGTCAGACG

    L  D  D  E  T  L  A  K  L  I  A  K  I  P  T  I  T  A  V  C  -

    AACTTGCATGGGGAGAAGCTACAGGTATTTAAGCAGTCTCATCCAGACATAGTGAATACA
661 ---------+---------+---------+---------+---------+---------+ 720
    TTGAACGTACCCCTCTTCGATGTCCATAAATTCGTCAGAGTAGGTCTGTATCACTTATGT

    N  L  H  G  E  K  L  Q  V  F  K  Q  S  H  P  D  I  V  N  T  -

    CTGTTTCCTCCATTGTACAAGGAGCTCTTTAATCCTGACTGTGCTGCGGTCTGCAAATGA
721 ---------+---------+---------+---------+---------+---------+ 780
    GACAAAGGAGGTAACATGTTCCTCGAGAAATTAGGACTGACACGACGCCAGACGTTTACT

    L  F  P  P  L  Y  K  E  L  F  N  P  D  C  A  A  V  C  K  *  -
```

FIGURE 2 (suite 1)

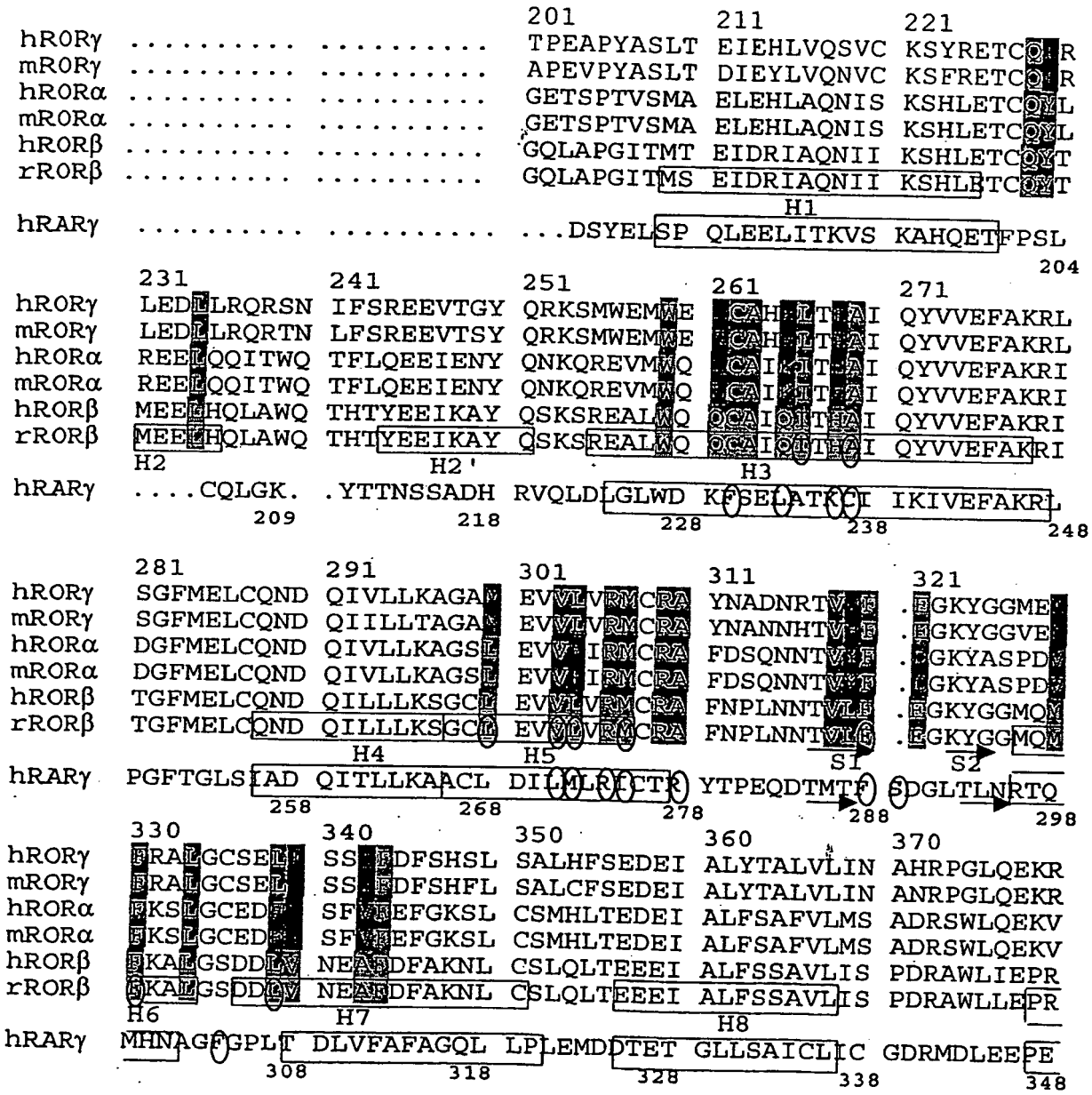

Figure 3

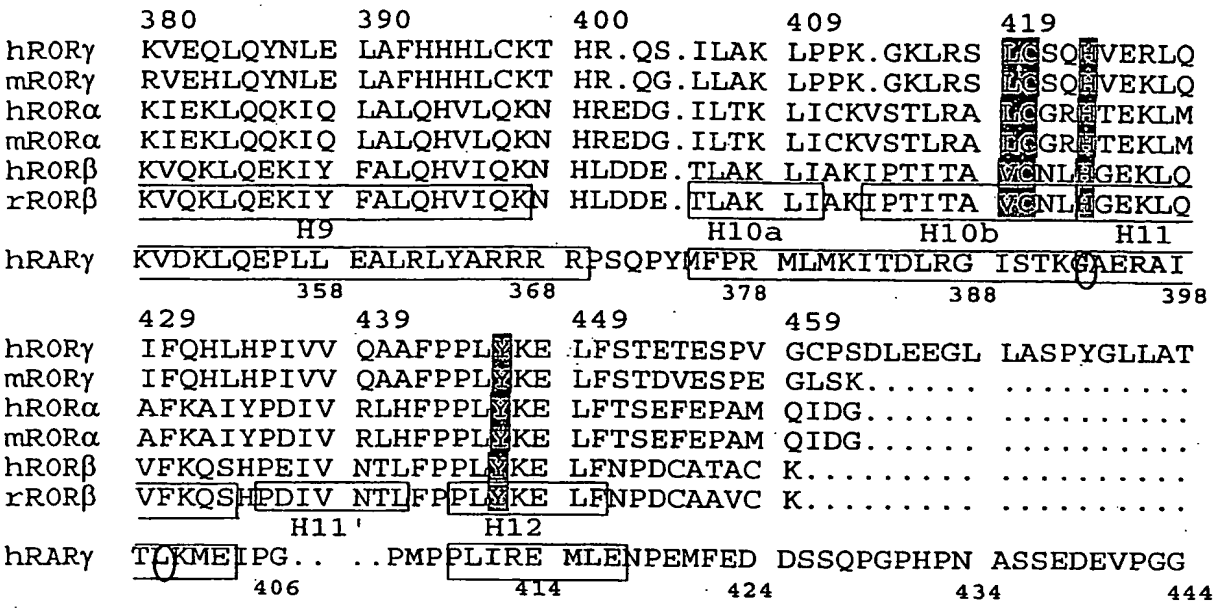

Figure 3 (suite 1)

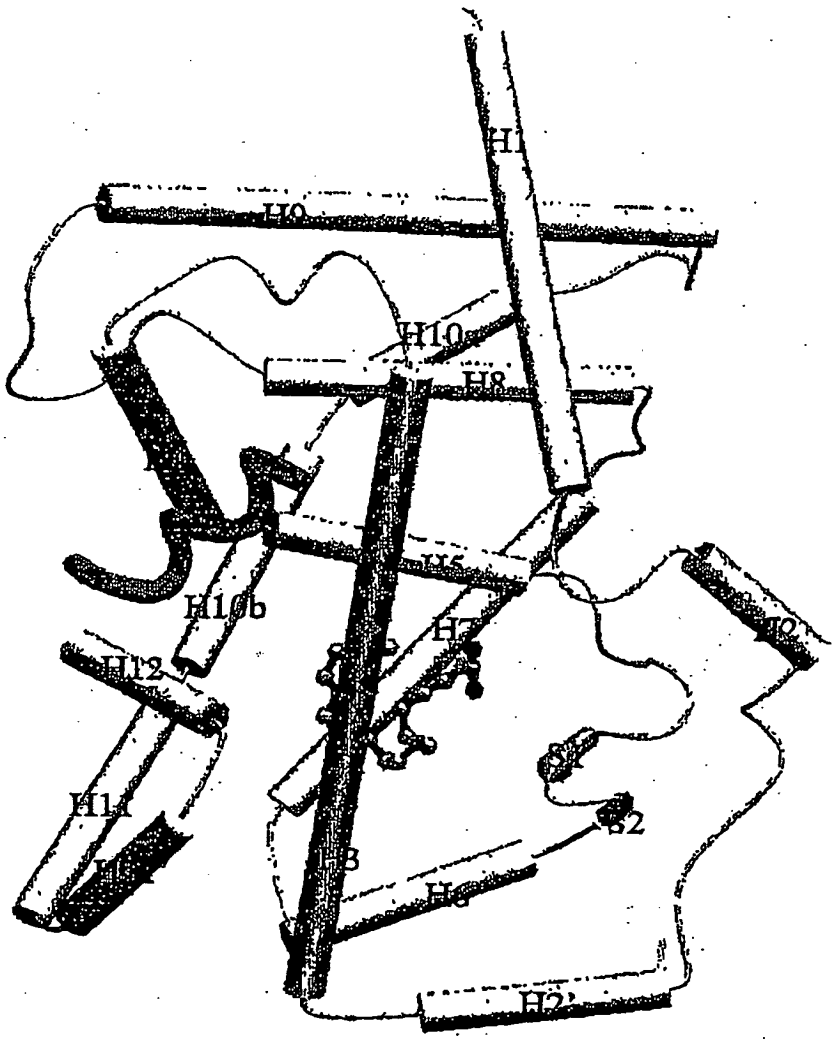

Figure 4

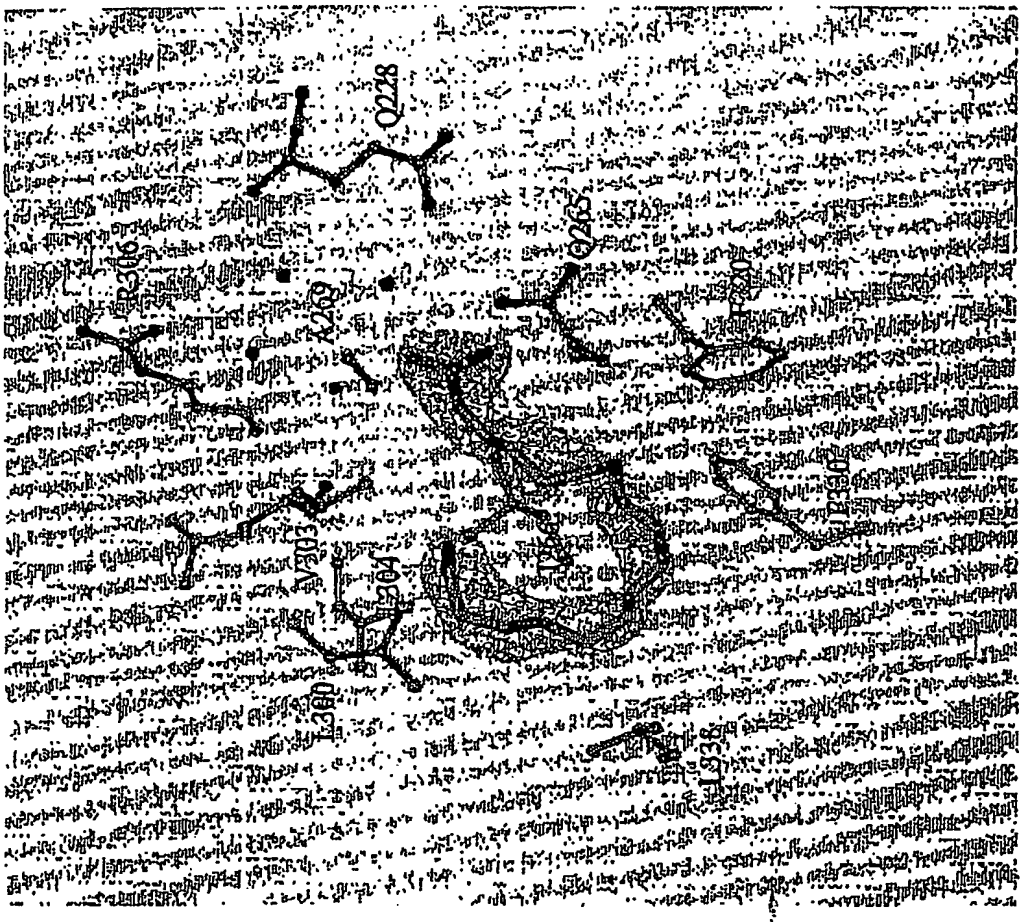

Figure 5

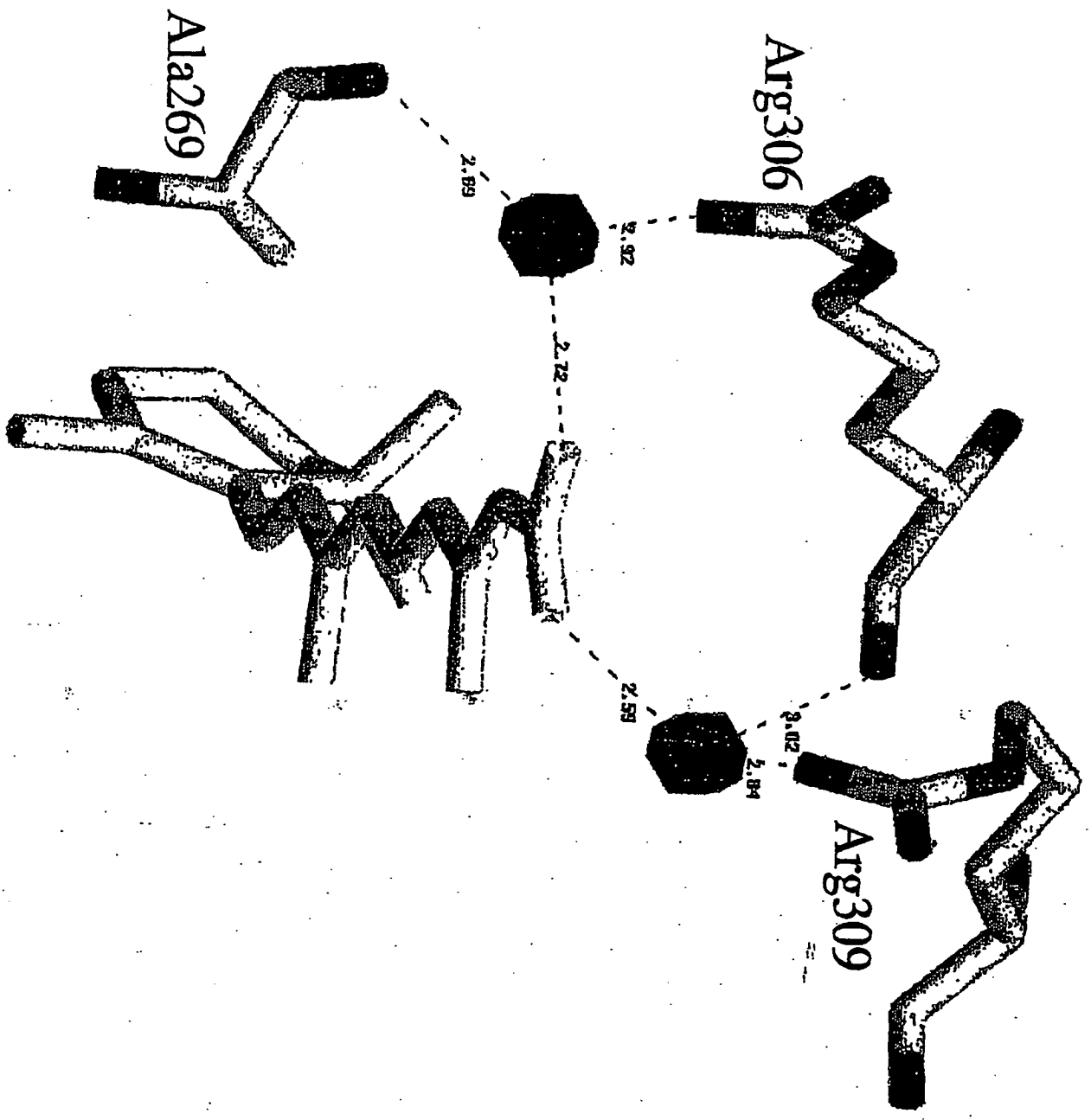

Figure 6

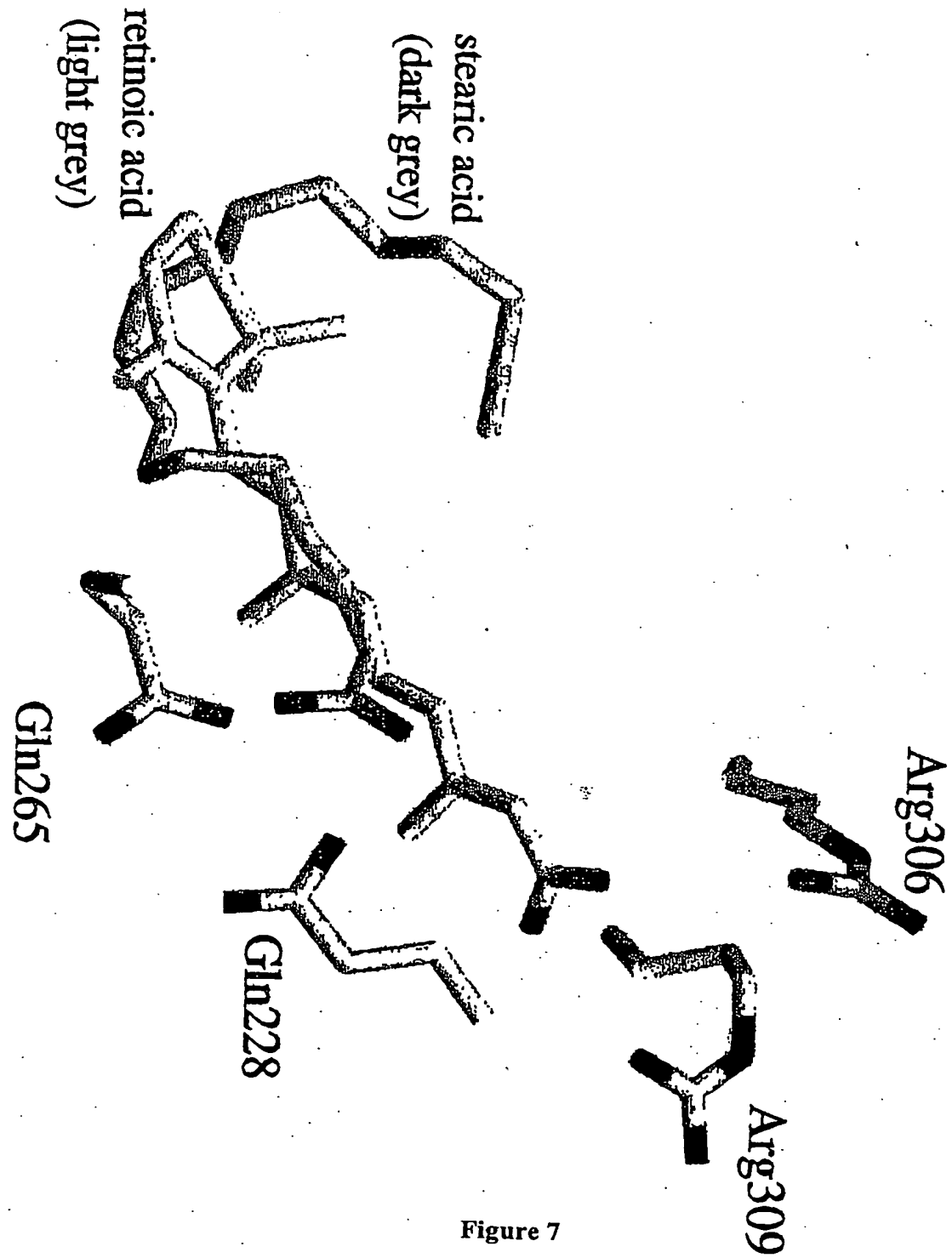

Figure 7

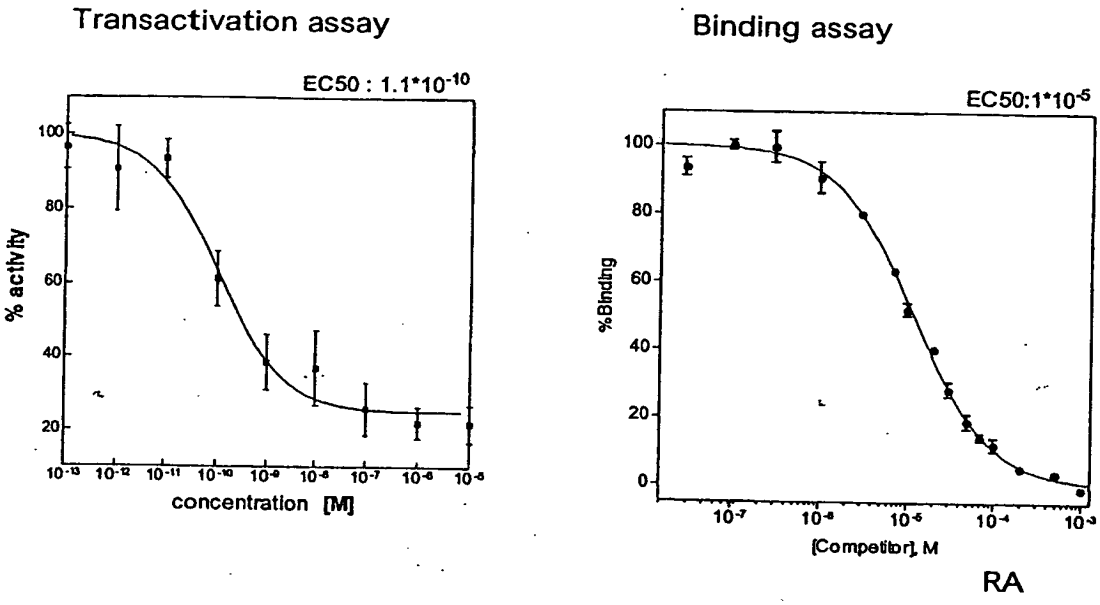

Figure 8

SEQUENCE LISTING

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<140>
<141>

<160> 37

<170> PatentIn Ver. 2.1

<210> 1
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleotide sequence coding for a fragment of rat RORβ

<220>
<221> CDS
<222> (1)..(732)

<400> 1

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atg tct gag atc gat cga att gca cag aac atc att aag tcc cat ttg   48
Met Ser Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His Leu
  1               5                  10                  15

gag acg tgc cag tac aca atg gaa gag ctc cat cag ctg gca tgg cag   96
Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp Gln
             20                  25                  30

acc cac acc tat gag gaa ata aag gca tat caa agc aag tcc agg gag   144
Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg Glu
         35                  40                  45

gct ctg tgg cag cag tgt gcc atc cag atc acc cac gcc atc caa tat   192
Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln Tyr
     50                  55                  60

gtg gtg gag ttc gca aag cgg ata aca ggc ttc atg gag ctg tgt cag   240
Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys Gln
 65                  70                  75                  80

aac gat cag atc tta ctt ctg aag tca ggt tgc ttg gaa gtg gtt tta   288
Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val Leu
                 85                  90                  95

gtg aga atg tgc cgt gcc ttc aac cca tta aac aac act gtt ctg ttt   336
Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu Phe
            100                 105                 110

gaa gga aaa tat gga gga atg caa atg ttc aaa gcc tta ggt tct gat   384
Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser Asp
        115                 120                 125
```

```
gac cta gtg aat gaa gca ttt gac ttt gcg aag aat ctg tgt tcc ttg   432
Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser Leu
    130                 135                 140

cag ctg acc gag gaa gag att gct ctg ttc tcc tct gct gtt ctg ata   480
Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu Ile
145                 150                 155                 160

tcc cca gac cga gcc tgg ctg tta gaa cca aga aaa gtc cag aag ctt   528
Ser Pro Asp Arg Ala Trp Leu Leu Glu Pro Arg Lys Val Gln Lys Leu
                165                 170                 175

cag gaa aaa att tat ttt gca ctt caa cat gtg att cag aag aat cac   576
Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn His
            180                 185                 190

ctg gat gat gag acc ctg gca aag tta ata gcc aag ata cca act atc   624
Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr Ile
        195                 200                 205

acg gca gtc tgc aac ttg cat ggg gag aag cta cag gta ttt aag cag   672
Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys Gln
    210                 215                 220

tct cat cca gac ata gtg aat aca ctg ttt cct cca ttg tac aag gag   720
Ser His Pro Asp Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys Glu
225                 230                 235                 240

ctc ttt aat cct                                                  732
Leu Phe Asn Pro
```

<210> 2
<211> 244
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: nucleotide sequence coding for a fragment of rat RORβ

<400> 2

```
Met Ser Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His Leu
  1               5                  10                  15

Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp Gln
            20                  25                  30

Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg Glu
        35                  40                  45

Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln Tyr
    50                  55                  60

Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys Gln
65                  70                  75                  80

Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val Leu
                85                  90                  95

Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu Phe
            100                 105                 110
```

```
Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser Asp
        115                 120                 125

Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser Leu
    130                 135                 140

Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu Ile
145                 150                 155                 160

Ser Pro Asp Arg Ala Trp Leu Leu Glu Pro Arg Lys Val Gln Lys Leu
                165                 170                 175

Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn His
            180                 185                 190

Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr Ile
        195                 200                 205

Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys Gln
    210                 215                 220

Ser His Pro Asp Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys Glu
225                 230                 235                 240

Leu Phe Asn Pro
```

<210> 3
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORβ

<400> 3

```
Met Thr Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His Leu
  1               5                  10                  15

Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp Gln
            20                  25                  30

Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg Glu
        35                  40                  45

Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln Tyr
    50                  55                  60

Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys Gln
65                  70                  75                  80

Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val Leu
                85                  90                  95

Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu Phe
            100                 105                 110
```

Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser Asp
115 120 125

Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser Leu
130 135 140

Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu Ile
145 150 155 160

Ser Pro Asp Arg Ala Trp Leu Ile Glu Pro Arg Lys Val Gln Lys Leu
165 170 175

Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn His
180 185 190

Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr Ile
195 200 205

Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys Gln
210 215 220

Ser His Pro Glu Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys Glu
225 230 235 240

Leu Phe Asn Pro

<210> 4
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORγ

<400> 4
Leu Thr Glu Ile Glu His Leu Val Gln Ser Val Cys Lys Ser Tyr Arg
1 5 10 15

Glu Thr Cys Gln Leu Arg Leu Glu Asp Leu Leu Arg Gln Arg Ser Asn
20 25 30

Ile Phe Ser Arg Glu Glu Val Thr Gly Tyr Gln Arg Lys Ser Met Trp
35 40 45

Glu Met Trp Glu Arg Cys Ala His His Leu Thr Glu Ala Ile Gln Tyr
50 55 60

Val Val Glu Phe Ala Lys Arg Leu Ser Gly Phe Met Glu Leu Cys Gln
65 70 75 80

Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ala Met Glu Val Val Leu
85 90 95

Val Arg Met Cys Arg Ala Tyr Asn Ala Asp Asn Arg Thr Val Phe Phe
100 105 110

Glu Gly Lys Tyr Gly Gly Met Glu Leu Phe Arg Ala Leu Gly Cys Ser
115 120 125

```
Glu Leu Ile Ser Ser Ile Phe Asp Phe Ser His Ser Leu Ser Ala Leu
    130                 135                 140

His Phe Ser Glu Asp Glu Ile Ala Leu Tyr Thr Ala Leu Val Leu Ile
145                 150                 155                 160

Asn Ala His Arg Pro Gly Leu Gln Glu Lys Arg Lys Val Glu Gln Leu
                165                 170                 175

Gln Tyr Asn Leu Glu Leu Ala Phe His His His Leu Cys Lys Thr His
            180                 185                 190

Arg Gln Ser Ile Leu Ala Lys Leu Pro Pro Lys Gly Lys Leu Arg Ser
        195                 200                 205

Leu Cys Ser Gln His Val Glu Arg Leu Gln Ile Phe Gln His Leu His
    210                 215                 220

Pro Ile Val Val Gln Ala Ala Phe Pro Pro Leu Tyr Lys Glu Leu Phe
225                 230                 235                 240

Ser Thr
```

<210> 5
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORγ

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<400> 5
Leu Thr Asp Ile Glu Tyr Leu Val Gln Asn Val Cys Lys Ser Phe Arg
  1               5                  10                  15

Glu Thr Cys Gln Leu Arg Leu Glu Asp Leu Leu Arg Gln Arg Thr Asn
            20                  25                  30

Leu Phe Ser Arg Glu Glu Val Thr Ser Tyr Gln Arg Lys Ser Met Trp
        35                  40                  45

Glu Met Trp Glu Arg Cys Ala His His Leu Thr Glu Ala Ile Gln Tyr
    50                  55                  60

Val Val Glu Phe Ala Lys Arg Leu Ser Gly Phe Met Glu Leu Cys Gln
65                  70                  75                  80

Asn Asp Gln Ile Ile Leu Leu Thr Ala Gly Ala Met Glu Val Val Leu
                85                  90                  95

Val Arg Met Cys Arg Ala Tyr Asn Ala Asn Asn His Thr Val Phe Phe
            100                 105                 110

Glu Gly Lys Tyr Gly Gly Val Glu Leu Phe Arg Ala Leu Gly Cys Ser
        115                 120                 125
```

```
Glu Leu Ile Ser Ser Ile Phe Asp Phe Ser His Phe Leu Ser Ala Leu
     130                 135                 140

Cys Phe Ser Glu Asp Glu Ile Ala Leu Tyr Thr Ala Leu Val Leu Ile
145                 150                 155                 160

Asn Ala Asn Arg Pro Gly Leu Gln Glu Lys Arg Arg Val Glu His Leu
                165                 170                 175

Gln Tyr Asn Leu Glu Leu Ala Phe His His His Leu Cys Lys Thr His
            180                 185                 190

Arg Gln Gly Leu Leu Ala Lys Leu Pro Pro Lys Gly Lys Leu Arg Ser
        195                 200                 205

Leu Cys Ser Gln His Val Glu Lys Leu Gln Ile Phe Gln His Leu His
    210                 215                 220

Pro Ile Val Val Gln Ala Ala Phe Pro Pro Leu Tyr Lys Glu Leu Phe
225                 230                 235                 240

Ser Thr
```

<210> 6
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORα

<400> 6

```
Met Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His Leu
  1               5                  10                  15

Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp Gln
            20                  25                  30

Thr Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg Glu
        35                  40                  45

Val Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln Tyr
    50                  55                  60

Val Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys Gln
65                  70                  75                  80

Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val Phe
                85                  90                  95

Ile Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr Phe
            100                 105                 110

Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys Glu
        115                 120                 125

Asp Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser Met
    130                 135                 140
```

```
His Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu Met
145                 150                 155                 160

Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu
                165                 170                 175

Gln Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn His
            180                 185                 190

Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu
        195                 200                 205

Arg Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala
    210                 215                 220

Ile Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu
225                 230                 235                 240

Leu Phe Thr Ser
```

<210> 7
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORα

<400> 13

```
Met Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His Leu
  1               5                  10                  15

Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp Gln
             20                  25                  30

Thr Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg Glu
         35                  40                  45

Val Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln Tyr
     50                  55                  60

Val Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys Gln
 65                  70                  75                  80

Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val Phe
                 85                  90                  95

Ile Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr Phe
            100                 105                 110

Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys Glu
        115                 120                 125

Asp Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser Met
    130                 135                 140
```

```
His Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu Met
145                 150                 155                 160

Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu
                165                 170                 175

Gln Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn His
            180                 185                 190

Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu
        195                 200                 205

Arg Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala
    210                 215                 220

Ile Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu
225                 230                 235                 240

Leu Phe Thr Ser
```

<210> 8
<211> 245
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: nucleotide sequence coding for a fragment of rat RORβ

<400> 8

```
Thr Met Ser Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His
  1               5                  10                  15

Leu Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp
            20                  25                  30

Gln Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg
        35                  40                  45

Glu Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln
    50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys
65                  70                  75                  80

Gln Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val
                85                  90                  95

Leu Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu
            100                 105                 110

Phe Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser
        115                 120                 125

Asp Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser
    130                 135                 140

Leu Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu
145                 150                 155                 160
```

```
Ile Ser Pro Asp Arg Ala Trp Leu Leu Glu Pro Arg Lys Val Gln Lys
                165                 170                 175

Leu Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn
            180                 185                 190

His Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr
        195                 200                 205

Ile Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys
    210                 215                 220

Gln Ser His Pro Asp Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys
225                 230                 235                 240

Glu Leu Phe Asn Pro
```

<210> 9
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORβ

<400> 9

```
Thr Met Thr Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His
  1               5                  10                  15

Leu Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp
            20                  25                  30

Gln Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg
        35                  40                  45

Glu Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln
    50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys
65                  70                  75                  80

Gln Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val
                85                  90                  95

Leu Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu
            100                 105                 110

Phe Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser
        115                 120                 125

Asp Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser
    130                 135                 140

Leu Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu
145                 150                 155                 160

Ile Ser Pro Asp Arg Ala Trp Leu Ile Glu Pro Arg Lys Val Gln Lys
                165                 170                 175
```

Leu Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn
180 185 190

His Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr
195 200 205

Ile Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys
210 215 220

Gln Ser His Pro Glu Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys
225 230 235 240

Glu Leu Phe Asn Pro

<210> 10
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORγ

<400> 10
Ser Leu Thr Glu Ile Glu His Leu Val Gln Ser Val Cys Lys Ser Tyr
1 5 10 15

Arg Glu Thr Cys Gln Leu Arg Leu Glu Asp Leu Leu Arg Gln Arg Ser
20 25 30

Asn Ile Phe Ser Arg Glu Glu Val Thr Gly Tyr Gln Arg Lys Ser Met
35 40 45

Trp Glu Met Trp Glu Arg Cys Ala His His Leu Thr Glu Ala Ile Gln
50 55 60

Tyr Val Val Glu Phe Ala Lys Arg Leu Ser Gly Phe Met Glu Leu Cys
65 70 75 80

Gln Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ala Met Glu Val Val
85 90 95

Leu Val Arg Met Cys Arg Ala Tyr Asn Ala Asp Asn Arg Thr Val Phe
100 105 110

Phe Glu Gly Lys Tyr Gly Gly Met Glu Leu Phe Arg Ala Leu Gly Cys
115 120 125

Ser Glu Leu Ile Ser Ser Ile Phe Asp Phe Ser His Ser Leu Ser Ala
130 135 140

Leu His Phe Ser Glu Asp Glu Ile Ala Leu Tyr Thr Ala Leu Val Leu
145 150 155 160

Ile Asn Ala His Arg Pro Gly Leu Gln Glu Lys Arg Lys Val Glu Gln
165 170 175

```
Leu Gln Tyr Asn Leu Glu Leu Ala Phe His His His Leu Cys Lys Thr
            180                 185                 190

His Arg Gln Ser Ile Leu Ala Lys Leu Pro Pro Lys Gly Lys Leu Arg
        195                 200                 205

Ser Leu Cys Ser Gln His Val Glu Arg Leu Gln Ile Phe Gln His Leu
    210                 215                 220

His Pro Ile Val Val Gln Ala Ala Phe Pro Pro Leu Tyr Lys Glu Leu
225                 230                 235                 240

Phe Ser Thr
```

<210> 11
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORγ

<400> 11

```
Ser Leu Thr Asp Ile Glu Tyr Leu Val Gln Asn Val Cys Lys Ser Phe
  1               5                  10                  15

Arg Glu Thr Cys Gln Leu Arg Leu Glu Asp Leu Leu Arg Gln Arg Thr
            20                  25                  30

Asn Leu Phe Ser Arg Glu Glu Val Thr Ser Tyr Gln Arg Lys Ser Met
        35                  40                  45

Trp Glu Met Trp Glu Arg Cys Ala His His Leu Thr Glu Ala Ile Gln
    50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Leu Ser Gly Phe Met Glu Leu Cys
65                  70                  75                  80

Gln Asn Asp Gln Ile Ile Leu Leu Thr Ala Gly Ala Met Glu Val Val
                85                  90                  95

Leu Val Arg Met Cys Arg Ala Tyr Asn Ala Asn Asn His Thr Val Phe
            100                 105                 110

Phe Glu Gly Lys Tyr Gly Gly Val Glu Leu Phe Arg Ala Leu Gly Cys
        115                 120                 125

Ser Glu Leu Ile Ser Ser Ile Phe Asp Phe Ser His Phe Leu Ser Ala
    130                 135                 140

Leu Cys Phe Ser Glu Asp Glu Ile Ala Leu Tyr Thr Ala Leu Val Leu
145                 150                 155                 160

Ile Asn Ala Asn Arg Pro Gly Leu Gln Glu Lys Arg Arg Val Glu His
                165                 170                 175

Leu Gln Tyr Asn Leu Glu Leu Ala Phe His His His Leu Cys Lys Thr
            180                 185                 190
```

```
His Arg Gln Gly Leu Leu Ala Lys Leu Pro Pro Lys Gly Lys Leu Arg
        195                 200                 205

Ser Leu Cys Ser Gln His Val Glu Lys Leu Gln Ile Phe Gln His Leu
    210                 215                 220

His Pro Ile Val Val Gln Ala Ala Phe Pro Pro Leu Tyr Lys Glu Leu
225                 230                 235                 240

Phe Ser Thr
```

<210> 12
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORα

<400> 12

```
Ser Met Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His
  1               5                  10                  15

Leu Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp
             20                  25                  30

Gln Thr Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg
         35                  40                  45

Glu Val Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln
     50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys
 65                  70                  75                  80

Gln Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val
                 85                  90                  95

Phe Ile Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr
            100                 105                 110

Phe Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys
        115                 120                 125

Glu Asp Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser
    130                 135                 140

Met His Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu
145                 150                 155                 160

Met Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys
                165                 170                 175

Leu Gln Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn
            180                 185                 190
```

```
His Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr
        195                 200                 205

Leu Arg Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys
    210                 215                 220

Ala Ile Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys
225                 230                 235                 240

Glu Leu Phe Thr Ser
```

<210> 13
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORα

<400> 13

```
Ser Met Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His
  1               5                  10                  15

Leu Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp
             20                  25                  30

Gln Thr Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg
         35                  40                  45

Glu Val Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln
     50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys
 65                  70                  75                  80

Gln Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val
                 85                  90                  95

Phe Ile Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr
            100                 105                 110

Phe Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys
        115                 120                 125

Glu Asp Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser
    130                 135                 140

Met His Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu
145                 150                 155                 160

Met Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys
                165                 170                 175

Leu Gln Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn
            180                 185                 190

His Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr
        195                 200                 205
```

Leu Arg Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys
210 215 220

Ala Ile Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys
225 230 235 240

Glu Leu Phe Thr Ser
245

<210> 14
<211> 244
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: nucleotide sequence coding for a fragment of rat RORβ

<400> 14
Thr Met Ser Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His
1 5 10 15

Leu Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp
20 25 30

Gln Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg
35 40 45

Glu Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln
50 55 60

Tyr Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys
65 70 75 80

Gln Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val
85 90 95

Leu Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu
100 105 110

Phe Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser
115 120 125

Asp Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser
130 135 140

Leu Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu
145 150 155 160

Ile Ser Pro Asp Arg Ala Trp Leu Leu Glu Pro Arg Lys Val Gln Lys
165 170 175

Leu Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn
180 185 190

His Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr
195 200 205

Ile Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys
210 215 220

```
Gln Ser His Pro Asp Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys
225                 230                 235                 240

Glu Leu Phe Asn
```

<210> 15
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORβ

<400> 15

```
Thr Met Thr Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His
  1               5                  10                  15

Leu Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp
             20                  25                  30

Gln Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg
         35                  40                  45

Glu Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln
     50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys
 65                  70                  75                  80

Gln Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val
                 85                  90                  95

Leu Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu
            100                 105                 110

Phe Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser
        115                 120                 125

Asp Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser
    130                 135                 140

Leu Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu
145                 150                 155                 160

Ile Ser Pro Asp Arg Ala Trp Leu Ile Glu Pro Arg Lys Val Gln Lys
                165                 170                 175

Leu Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn
            180                 185                 190

His Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr
        195                 200                 205

Ile Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys
    210                 215                 220

Gln Ser His Pro Glu Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys
225                 230                 235                 240
```

Glu Leu Phe Asn

<210> 16
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORγ

<400> 16

```
Ser Leu Thr Glu Ile Glu His Leu Val Gln Ser Val Cys Lys Ser Tyr
  1               5                  10                  15

Arg Glu Thr Cys Gln Leu Arg Leu Glu Asp Leu Leu Arg Gln Arg Ser
             20                  25                  30

Asn Ile Phe Ser Arg Glu Glu Val Thr Gly Tyr Gln Arg Lys Ser Met
         35                  40                  45

Trp Glu Met Trp Glu Arg Cys Ala His His Leu Thr Glu Ala Ile Gln
     50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Leu Ser Gly Phe Met Glu Leu Cys
 65                  70                  75                  80

Gln Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ala Met Glu Val Val
                 85                  90                  95

Leu Val Arg Met Cys Arg Ala Tyr Asn Ala Asp Asn Arg Thr Val Phe
            100                 105                 110

Phe Glu Gly Lys Tyr Gly Gly Met Glu Leu Phe Arg Ala Leu Gly Cys
        115                 120                 125

Ser Glu Leu Ile Ser Ser Ile Phe Asp Phe Ser His Ser Leu Ser Ala
    130                 135                 140

Leu His Phe Ser Glu Asp Glu Ile Ala Leu Tyr Thr Ala Leu Val Leu
145                 150                 155                 160

Ile Asn Ala His Arg Pro Gly Leu Gln Glu Lys Arg Lys Val Glu Gln
                165                 170                 175

Leu Gln Tyr Asn Leu Glu Leu Ala Phe His His His Leu Cys Lys Thr
            180                 185                 190

His Arg Gln Ser Ile Leu Ala Lys Leu Pro Pro Lys Gly Lys Leu Arg
        195                 200                 205

Ser Leu Cys Ser Gln His Val Glu Arg Leu Gln Ile Phe Gln His Leu
    210                 215                 220

His Pro Ile Val Val Gln Ala Ala Phe Pro Pro Leu Tyr Lys Glu Leu
225                 230                 235                 240

Phe Ser
```

<210> 17
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORγ

<400> 17

```
Ser Leu Thr Asp Ile Glu Tyr Leu Val Gln Asn Val Cys Lys Ser Phe
  1               5                  10                  15

Arg Glu Thr Cys Gln Leu Arg Leu Glu Asp Leu Leu Arg Gln Arg Thr
             20                  25                  30

Asn Leu Phe Ser Arg Glu Glu Val Thr Ser Tyr Gln Arg Lys Ser Met
         35                  40                  45

Trp Glu Met Trp Glu Arg Cys Ala His His Leu Thr Glu Ala Ile Gln
     50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Leu Ser Gly Phe Met Glu Leu Cys
 65                  70                  75                  80

Gln Asn Asp Gln Ile Ile Leu Leu Thr Ala Gly Ala Met Glu Val Val
                 85                  90                  95

Leu Val Arg Met Cys Arg Ala Tyr Asn Ala Asn Asn His Thr Val Phe
            100                 105                 110

Phe Glu Gly Lys Tyr Gly Gly Val Glu Leu Phe Arg Ala Leu Gly Cys
        115                 120                 125

Ser Glu Leu Ile Ser Ser Ile Phe Asp Phe Ser His Phe Leu Ser Ala
    130                 135                 140

Leu Cys Phe Ser Glu Asp Glu Ile Ala Leu Tyr Thr Ala Leu Val Leu
145                 150                 155                 160

Ile Asn Ala Asn Arg Pro Gly Leu Gln Glu Lys Arg Arg Val Glu His
                165                 170                 175

Leu Gln Tyr Asn Leu Glu Leu Ala Phe His His His Leu Cys Lys Thr
            180                 185                 190

His Arg Gln Gly Leu Leu Ala Lys Leu Pro Pro Lys Gly Lys Leu Arg
        195                 200                 205

Ser Leu Cys Ser Gln His Val Glu Lys Leu Gln Ile Phe Gln His Leu
    210                 215                 220

His Pro Ile Val Val Gln Ala Ala Phe Pro Pro Leu Tyr Lys Glu Leu
225                 230                 235                 240

Phe Ser
```

<210> 18
<211> 244

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORα

<400> 18

```
Ser Met Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His
  1               5                  10                  15

Leu Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp
             20                  25                  30

Gln Thr Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg
         35                  40                  45

Glu Val Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln
     50                  55                  60

Tyr Val Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys
 65                  70                  75                  80

Gln Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val
                 85                  90                  95

Phe Ile Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr
            100                 105                 110

Phe Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys
        115                 120                 125

Glu Asp Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser
    130                 135                 140

Met His Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu
145                 150                 155                 160

Met Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys
                165                 170                 175

Leu Gln Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn
            180                 185                 190

His Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr
        195                 200                 205

Leu Arg Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys
    210                 215                 220

Ala Ile Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys
225                 230                 235                 240

Glu Leu Phe Thr
```

<210> 19
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORα

<400> 19
Ser Met Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His
1 5 10 15

Leu Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp
20 25 30

Gln Thr Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg
35 40 45

Glu Val Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln
50 55 60

Tyr Val Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys
65 70 75 80

Gln Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val
85 90 95

Phe Ile Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr
100 105 110

Phe Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys
115 120 125

Glu Asp Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser
130 135 140

Met His Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu
145 150 155 160

Met Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys
165 170 175

Leu Gln Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn
180 185 190

His Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr
195 200 205

Leu Arg Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys
210 215 220

Ala Ile Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys
225 230 235 240

Glu Leu Phe Thr

<210> 20
<211> 243
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: nucleotide sequence coding for a fragment of rat RORβ

<400> 20

```
Met Ser Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His Leu
  1               5                  10                  15

Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp Gln
             20                  25                  30

Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg Glu
         35                  40                  45

Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln Tyr
     50                  55                  60

Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys Gln
 65                  70                  75                  80

Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val Leu
                 85                  90                  95

Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu Phe
            100                 105                 110

Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser Asp
        115                 120                 125

Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser Leu
    130                 135                 140

Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu Ile
145                 150                 155                 160

Ser Pro Asp Arg Ala Trp Leu Leu Glu Pro Arg Lys Val Gln Lys Leu
                165                 170                 175

Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn His
            180                 185                 190

Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr Ile
        195                 200                 205

Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys Gln
    210                 215                 220

Ser His Pro Asp Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys Glu
225                 230                 235                 240

Leu Phe Asn
```

<210> 21
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORβ

<400> 21

```
Met Thr Glu Ile Asp Arg Ile Ala Gln Asn Ile Ile Lys Ser His Leu
  1               5                  10                  15

Glu Thr Cys Gln Tyr Thr Met Glu Glu Leu His Gln Leu Ala Trp Gln
             20                  25                  30

Thr His Thr Tyr Glu Glu Ile Lys Ala Tyr Gln Ser Lys Ser Arg Glu
         35                  40                  45

Ala Leu Trp Gln Gln Cys Ala Ile Gln Ile Thr His Ala Ile Gln Tyr
     50                  55                  60

Val Val Glu Phe Ala Lys Arg Ile Thr Gly Phe Met Glu Leu Cys Gln
 65                  70                  75                  80

Asn Asp Gln Ile Leu Leu Leu Lys Ser Gly Cys Leu Glu Val Val Leu
                 85                  90                  95

Val Arg Met Cys Arg Ala Phe Asn Pro Leu Asn Asn Thr Val Leu Phe
            100                 105                 110

Glu Gly Lys Tyr Gly Gly Met Gln Met Phe Lys Ala Leu Gly Ser Asp
        115                 120                 125

Asp Leu Val Asn Glu Ala Phe Asp Phe Ala Lys Asn Leu Cys Ser Leu
    130                 135                 140

Gln Leu Thr Glu Glu Glu Ile Ala Leu Phe Ser Ser Ala Val Leu Ile
145                 150                 155                 160

Ser Pro Asp Arg Ala Trp Leu Ile Glu Pro Arg Lys Val Gln Lys Leu
                165                 170                 175

Gln Glu Lys Ile Tyr Phe Ala Leu Gln His Val Ile Gln Lys Asn His
            180                 185                 190

Leu Asp Asp Glu Thr Leu Ala Lys Leu Ile Ala Lys Ile Pro Thr Ile
        195                 200                 205

Thr Ala Val Cys Asn Leu His Gly Glu Lys Leu Gln Val Phe Lys Gln
    210                 215                 220

Ser His Pro Glu Ile Val Asn Thr Leu Phe Pro Pro Leu Tyr Lys Glu
225                 230                 235                 240

Leu Phe Asn
```

<210> 22
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORγ

<400> 22

```
Leu Thr Glu Ile Glu His Leu Val Gln Ser Val Cys Lys Ser Tyr Arg
  1               5                  10                  15
```

```
Glu Thr Cys Gln Leu Arg Leu Glu Asp Leu Leu Arg Gln Arg Ser Asn
            20                  25                  30

Ile Phe Ser Arg Glu Glu Val Thr Gly Tyr Gln Arg Lys Ser Met Trp
        35                  40                  45

Glu Met Trp Glu Arg Cys Ala His His Leu Thr Glu Ala Ile Gln Tyr
    50                  55                  60

Val Val Glu Phe Ala Lys Arg Leu Ser Gly Phe Met Glu Leu Cys Gln
65                  70                  75                  80

Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ala Met Glu Val Val Leu
                85                  90                  95

Val Arg Met Cys Arg Ala Tyr Asn Ala Asp Asn Arg Thr Val Phe Phe
            100                 105                 110

Glu Gly Lys Tyr Gly Gly Met Glu Leu Phe Arg Ala Leu Gly Cys Ser
        115                 120                 125

Glu Leu Ile Ser Ser Ile Phe Asp Phe Ser His Ser Leu Ser Ala Leu
    130                 135                 140

His Phe Ser Glu Asp Glu Ile Ala Leu Tyr Thr Ala Leu Val Leu Ile
145                 150                 155                 160

Asn Ala His Arg Pro Gly Leu Gln Glu Lys Arg Lys Val Glu Gln Leu
                165                 170                 175

Gln Tyr Asn Leu Glu Leu Ala Phe His His His Leu Cys Lys Thr His
            180                 185                 190

Arg Gln Ser Ile Leu Ala Lys Leu Pro Pro Lys Gly Lys Leu Arg Ser
        195                 200                 205

Leu Cys Ser Gln His Val Glu Arg Leu Gln Ile Phe Gln His Leu His
    210                 215                 220

Pro Ile Val Val Gln Ala Ala Phe Pro Pro Leu Tyr Lys Glu Leu Phe
225                 230                 235                 240

Ser
```

<210> 23
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORγ

<400> 23

```
Leu Thr Asp Ile Glu Tyr Leu Val Gln Asn Val Cys Lys Ser Phe Arg
  1               5                  10                  15
```

```
Glu Thr Cys Gln Leu Arg Leu Glu Asp Leu Leu Arg Gln Arg Thr Asn
            20                  25                  30

Leu Phe Ser Arg Glu Glu Val Thr Ser Tyr Gln Arg Lys Ser Met Trp
        35                  40                  45

Glu Met Trp Glu Arg Cys Ala His His Leu Thr Glu Ala Ile Gln Tyr
    50                  55                  60

Val Val Glu Phe Ala Lys Arg Leu Ser Gly Phe Met Glu Leu Cys Gln
65                  70                  75                  80

Asn Asp Gln Ile Ile Leu Leu Thr Ala Gly Ala Met Glu Val Val Leu
                85                  90                  95

Val Arg Met Cys Arg Ala Tyr Asn Ala Asn Asn His Thr Val Phe Phe
            100                 105                 110

Glu Gly Lys Tyr Gly Gly Val Glu Leu Phe Arg Ala Leu Gly Cys Ser
        115                 120                 125

Glu Leu Ile Ser Ser Ile Phe Asp Phe Ser His Phe Leu Ser Ala Leu
    130                 135                 140

Cys Phe Ser Glu Asp Glu Ile Ala Leu Tyr Thr Ala Leu Val Leu Ile
145                 150                 155                 160

Asn Ala Asn Arg Pro Gly Leu Gln Glu Lys Arg Arg Val Glu His Leu
                165                 170                 175

Gln Tyr Asn Leu Glu Leu Ala Phe His His His Leu Cys Lys Thr His
            180                 185                 190

Arg Gln Gly Leu Leu Ala Lys Leu Pro Pro Lys Gly Lys Leu Arg Ser
        195                 200                 205

Leu Cys Ser Gln His Val Glu Lys Leu Gln Ile Phe Gln His Leu His
    210                 215                 220

Pro Ile Val Val Gln Ala Ala Phe Pro Pro Leu Tyr Lys Glu Leu Phe
225                 230                 235                 240

Ser
```

<210> 24
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORα

<400> 24

```
Met Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His Leu
  1               5                  10                  15

Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp Gln
            20                  25                  30
```

```
Thr Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg Glu
         35                  40                  45

Val Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln Tyr
     50                  55                  60

Val Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys Gln
 65                  70                  75                  80

Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val Phe
                 85                  90                  95

Ile Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr Phe
            100                 105                 110

Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys Glu
        115                 120                 125

Asp Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser Met
    130                 135                 140

His Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu Met
145                 150                 155                 160

Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu
                165                 170                 175

Gln Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn His
            180                 185                 190

Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu
        195                 200                 205

Arg Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala
    210                 215                 220

Ile Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu
225                 230                 235                 240

Leu Phe Thr
```

<210> 25
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORα

<400> 25

```
Met Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His Leu
  1               5                  10                  15

Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp Gln
            20                  25                  30
```

Thr Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg Glu
35 40 45

Val Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln Tyr
50 55 60

Val Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys Gln
65 70 75 80

Asn Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val Phe
85 90 95

Ile Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr Phe
100 105 110

Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys Glu
115 120 125

Asp Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser Met
130 135 140

His Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu Met
145 150 155 160

Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu
165 170 175

Gln Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn His
180 185 190

Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu
195 200 205

Arg Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala
210 215 220

Ile Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu
225 230 235 240

Leu Phe Thr

<210> 26
<211> 251
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: nucleotide sequence coding for a fragment of rat RORβ

<400> 26
Gly Gln Leu Ala Pro Gly Ile Thr Met Ser Glu Ile Asp Arg Ile Ala
1 5 10 15

Gln Asn Ile Ile Lys Ser His Leu Glu Thr Cys Gln Tyr Thr Met Glu
20 25 30

Glu Leu His Gln Leu Ala Trp Gln Thr His Thr Tyr Glu Glu Ile Lys
35 40 45

Ala Tyr Gln Ser Lys Ser Arg Glu Ala Leu Trp Gln Gln Cys Ala Ile
50 55 60

```
Gln Ile Thr His Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile
 65                  70                  75                  80

Thr Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Leu Leu Leu Lys
                85                  90                  95

Ser Gly Cys Leu Glu Val Val Leu Val Arg Met Cys Arg Ala Phe Asn
            100                 105                 110

Pro Leu Asn Asn Thr Val Leu Phe Glu Gly Lys Tyr Gly Gly Met Gln
        115                 120                 125

Met Phe Lys Ala Leu Gly Ser Asp Asp Leu Val Asn Glu Ala Phe Asp
    130                 135                 140

Phe Ala Lys Asn Leu Cys Ser Leu Gln Leu Thr Glu Glu Glu Ile Ala
145                 150                 155                 160

Leu Phe Ser Ser Ala Val Leu Ile Ser Pro Asp Arg Ala Trp Leu Leu
                165                 170                 175

Glu Pro Arg Lys Val Gln Lys Leu Gln Glu Lys Ile Tyr Phe Ala Leu
            180                 185                 190

Gln His Val Ile Gln Lys Asn His Leu Asp Asp Glu Thr Leu Ala Lys
        195                 200                 205

Leu Ile Ala Lys Ile Pro Thr Ile Thr Ala Val Cys Asn Leu His Gly
    210                 215                 220

Glu Lys Leu Gln Val Phe Lys Gln Ser His Pro Asp Ile Val Asn Thr
225                 230                 235                 240

Leu Phe Pro Pro Leu Tyr Lys Glu Leu Phe Asn
                245                 250
```

<210> 27
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORβ

<400> 27

```
Gly Gln Leu Ala Pro Gly Ile Thr Met Thr Glu Ile Asp Arg Ile Ala
  1               5                  10                  15

Gln Asn Ile Ile Lys Ser His Leu Glu Thr Cys Gln Tyr Thr Met Glu
            20                  25                  30

Glu Leu His Gln Leu Ala Trp Gln Thr His Thr Tyr Glu Glu Ile Lys
        35                  40                  45

Ala Tyr Gln Ser Lys Ser Arg Glu Ala Leu Trp Gln Gln Cys Ala Ile
    50                  55                  60
```

```
Gln Ile Thr His Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile
 65                  70                  75                  80

Thr Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Leu Leu Leu Lys
                 85                  90                  95

Ser Gly Cys Leu Glu Val Val Leu Val Arg Met Cys Arg Ala Phe Asn
            100                 105                 110

Pro Leu Asn Asn Thr Val Leu Phe Glu Gly Lys Tyr Gly Gly Met Gln
        115                 120                 125

Met Phe Lys Ala Leu Gly Ser Asp Asp Leu Val Asn Glu Ala Phe Asp
    130                 135                 140

Phe Ala Lys Asn Leu Cys Ser Leu Gln Leu Thr Glu Glu Glu Ile Ala
145                 150                 155                 160

Leu Phe Ser Ser Ala Val Leu Ile Ser Pro Asp Arg Ala Trp Leu Ile
                165                 170                 175

Glu Pro Arg Lys Val Gln Lys Leu Gln Glu Lys Ile Tyr Phe Ala Leu
            180                 185                 190

Gln His Val Ile Gln Lys Asn His Leu Asp Asp Glu Thr Leu Ala Lys
        195                 200                 205

Leu Ile Ala Lys Ile Pro Thr Ile Thr Ala Val Cys Asn Leu His Gly
    210                 215                 220

Glu Lys Leu Gln Val Phe Lys Gln Ser His Pro Glu Ile Val Asn Thr
225                 230                 235                 240

Leu Phe Pro Pro Leu Tyr Lys Glu Leu Phe Asn
                245                 250
```

<210> 28
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORγ

<400> 28

```
Thr Pro Glu Ala Pro Tyr Ala Ser Leu Thr Glu Ile Glu His Leu Val
  1               5                  10                  15

Gln Ser Val Cys Lys Ser Tyr Arg Glu Thr Cys Gln Leu Arg Leu Glu
             20                  25                  30

Asp Leu Leu Arg Gln Arg Ser Asn Ile Phe Ser Arg Glu Glu Val Thr
         35                  40                  45

Gly Tyr Gln Arg Lys Ser Met Trp Glu Met Trp Glu Arg Cys Ala His
     50                  55                  60

His Leu Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Leu
 65                  70                  75                  80
```

```
Ser Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Val Leu Leu Lys
                85                  90                  95

Ala Gly Ala Met Glu Val Val Leu Val Arg Met Cys Arg Ala Tyr Asn
            100                 105                 110

Ala Asp Asn Arg Thr Val Phe Phe Glu Gly Lys Tyr Gly Gly Met Glu
        115                 120                 125

Leu Phe Arg Ala Leu Gly Cys Ser Glu Leu Ile Ser Ser Ile Phe Asp
    130                 135                 140

Phe Ser His Ser Leu Ser Ala Leu His Phe Ser Glu Asp Glu Ile Ala
145                 150                 155                 160

Leu Tyr Thr Ala Leu Val Leu Ile Asn Ala His Arg Pro Gly Leu Gln
                165                 170                 175

Glu Lys Arg Lys Val Glu Gln Leu Gln Tyr Asn Leu Glu Leu Ala Phe
            180                 185                 190

His His His Leu Cys Lys Thr His Arg Gln Ser Ile Leu Ala Lys Leu
        195                 200                 205

Pro Pro Lys Gly Lys Leu Arg Ser Leu Cys Ser Gln His Val Glu Arg
    210                 215                 220

Leu Gln Ile Phe Gln His Leu His Pro Ile Val Val Gln Ala Ala Phe
225                 230                 235                 240

Pro Pro Leu Tyr Lys Glu Leu Phe Ser
                245
```

<210> 29
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORγ

<400> 29

```
Ala Pro Glu Val Pro Tyr Ala Ser Leu Thr Asp Ile Glu Tyr Leu Val
  1               5                  10                  15

Gln Asn Val Cys Lys Ser Phe Arg Glu Thr Cys Gln Leu Arg Leu Glu
            20                  25                  30

Asp Leu Leu Arg Gln Arg Thr Asn Leu Phe Ser Arg Glu Glu Val Thr
        35                  40                  45

Ser Tyr Gln Arg Lys Ser Met Trp Glu Met Trp Glu Arg Cys Ala His
    50                  55                  60

His Leu Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Leu
65                  70                  75                  80
```

Ser Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Ile Leu Leu Thr
85 90 95

Ala Gly Ala Met Glu Val Val Leu Val Arg Met Cys Arg Ala Tyr Asn
100 105 110

Ala Asn Asn His Thr Val Phe Phe Glu Gly Lys Tyr Gly Gly Val Glu
115 120 125

Leu Phe Arg Ala Leu Gly Cys Ser Glu Leu Ile Ser Ser Ile Phe Asp
130 135 140

Phe Ser His Phe Leu Ser Ala Leu Cys Phe Ser Glu Asp Glu Ile Ala
145 150 155 160

Leu Tyr Thr Ala Leu Val Leu Ile Asn Ala Asn Arg Pro Gly Leu Gln
165 170 175

Glu Lys Arg Arg Val Glu His Leu Gln Tyr Asn Leu Glu Leu Ala Phe
180 185 190

His His His Leu Cys Lys Thr His Arg Gln Gly Leu Leu Ala Lys Leu
195 200 205

Pro Pro Lys Gly Lys Leu Arg Ser Leu Cys Ser Gln His Val Glu Lys
210 215 220

Leu Gln Ile Phe Gln His Leu His Pro Ile Val Val Gln Ala Ala Phe
225 230 235 240

Pro Pro Leu Tyr Lys Glu Leu Phe Ser
245

<210> 30
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORα

<400> 30
Gly Glu Thr Ser Pro Thr Val Ser Met Ala Glu Leu Glu His Leu Ala
1 5 10 15

Gln Asn Ile Ser Lys Ser His Leu Glu Thr Cys Gln Tyr Leu Arg Glu
20 25 30

Glu Leu Gln Gln Ile Thr Trp Gln Thr Phe Leu Gln Glu Glu Ile Glu
35 40 45

Asn Tyr Gln Asn Lys Gln Arg Glu Val Met Trp Gln Leu Cys Ala Ile
50 55 60

Lys Ile Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile
65 70 75 80

Asp Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Val Leu Leu Lys
85 90 95

Ala Gly Ser Leu Glu Val Val Phe Ile Arg Met Cys Arg Ala Phe Asp
100 105 110

Ser Gln Asn Asn Thr Val Tyr Phe Asp Gly Lys Tyr Ala Ser Pro Asp
115 120 125

Val Phe Lys Ser Leu Gly Cys Glu Asp Phe Ile Ser Phe Val Phe Glu
130 135 140

Phe Gly Lys Ser Leu Cys Ser Met His Leu Thr Glu Asp Glu Ile Ala
145 150 155 160

Leu Phe Ser Ala Phe Val Leu Met Ser Ala Asp Arg Ser Trp Leu Gln
165 170 175

Glu Lys Val Lys Ile Glu Lys Leu Gln Gln Lys Ile Gln Leu Ala Leu
180 185 190

Gln His Val Leu Gln Lys Asn His Arg Glu Asp Gly Ile Leu Thr Lys
195 200 205

Leu Ile Cys Lys Val Ser Thr Leu Arg Ala Leu Cys Gly Arg His Thr
210 215 220

Glu Lys Leu Met Ala Phe Lys Ala Ile Tyr Pro Asp Ile Val Arg Leu
225 230 235 240

His Phe Pro Pro Leu Tyr Lys Glu Leu Phe Thr
245 250

<210> 31
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORα

<400> 31
Gly Glu Thr Ser Pro Thr Val Ser Met Ala Glu Leu Glu His Leu Ala
1 5 10 15

Gln Asn Ile Ser Lys Ser His Leu Glu Thr Cys Gln Tyr Leu Arg Glu
20 25 30

Glu Leu Gln Gln Ile Thr Trp Gln Thr Phe Leu Gln Glu Glu Ile Glu
35 40 45

Asn Tyr Gln Asn Lys Gln Arg Glu Val Met Trp Gln Leu Cys Ala Ile
50 55 60

Lys Ile Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile
65 70 75 80

Asp Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Val Leu Leu Lys
85 90 95

```
Ala Gly Ser Leu Glu Val Val Phe Ile Arg Met Cys Arg Ala Phe Asp
            100                 105                 110

Ser Gln Asn Asn Thr Val Tyr Phe Asp Gly Lys Tyr Ala Ser Pro Asp
        115                 120                 125

Val Phe Lys Ser Leu Gly Cys Glu Asp Phe Ile Ser Phe Val Phe Glu
    130                 135                 140

Phe Gly Lys Ser Leu Cys Ser Met His Leu Thr Glu Asp Glu Ile Ala
145                 150                 155                 160

Leu Phe Ser Ala Phe Val Leu Met Ser Ala Asp Arg Ser Trp Leu Gln
                165                 170                 175

Glu Lys Val Lys Ile Glu Lys Leu Gln Gln Lys Ile Gln Leu Ala Leu
            180                 185                 190

Gln His Val Leu Gln Lys Asn His Arg Glu Asp Gly Ile Leu Thr Lys
        195                 200                 205

Leu Ile Cys Lys Val Ser Thr Leu Arg Ala Leu Cys Gly Arg His Thr
    210                 215                 220

Glu Lys Leu Met Ala Phe Lys Ala Ile Tyr Pro Asp Ile Val Arg Leu
225                 230                 235                 240

His Phe Pro Pro Leu Tyr Lys Glu Leu Phe Thr
                245                 250
```

<210> 32
<211> 252
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: nucleotide sequence coding for a fragment of rat RORβ

<400> 32

```
Gly Gln Leu Ala Pro Gly Ile Thr Met Ser Glu Ile Asp Arg Ile Ala
  1               5                  10                  15

Gln Asn Ile Ile Lys Ser His Leu Glu Thr Cys Gln Tyr Thr Met Glu
             20                  25                  30

Glu Leu His Gln Leu Ala Trp Gln Thr His Thr Tyr Glu Glu Ile Lys
         35                  40                  45

Ala Tyr Gln Ser Lys Ser Arg Glu Ala Leu Trp Gln Gln Cys Ala Ile
     50                  55                  60

Gln Ile Thr His Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile
 65                  70                  75                  80

Thr Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Leu Leu Leu Lys
                 85                  90                  95

Ser Gly Cys Leu Glu Val Val Leu Val Arg Met Cys Arg Ala Phe Asn
            100                 105                 110
```

Pro Leu Asn Asn Thr Val Leu Phe Glu Gly Lys Tyr Gly Gly Met Gln
115 120 125

Met Phe Lys Ala Leu Gly Ser Asp Asp Leu Val Asn Glu Ala Phe Asp
130 135 140

Phe Ala Lys Asn Leu Cys Ser Leu Gln Leu Thr Glu Glu Glu Ile Ala
145 150 155 160

Leu Phe Ser Ser Ala Val Leu Ile Ser Pro Asp Arg Ala Trp Leu Leu
165 170 175

Glu Pro Arg Lys Val Gln Lys Leu Gln Glu Lys Ile Tyr Phe Ala Leu
180 185 190

Gln His Val Ile Gln Lys Asn His Leu Asp Asp Glu Thr Leu Ala Lys
195 200 205

Leu Ile Ala Lys Ile Pro Thr Ile Thr Ala Val Cys Asn Leu His Gly
210 215 220

Glu Lys Leu Gln Val Phe Lys Gln Ser His Pro Asp Ile Val Asn Thr
225 230 235 240

Leu Phe Pro Pro Leu Tyr Lys Glu Leu Phe Asn Pro
245 250

<210> 33
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORβ

<400> 33
Gly Gln Leu Ala Pro Gly Ile Thr Met Thr Glu Ile Asp Arg Ile Ala
1 5 10 15

Gln Asn Ile Ile Lys Ser His Leu Glu Thr Cys Gln Tyr Thr Met Glu
20 25 30

Glu Leu His Gln Leu Ala Trp Gln Thr His Thr Tyr Glu Glu Ile Lys
35 40 45

Ala Tyr Gln Ser Lys Ser Arg Glu Ala Leu Trp Gln Gln Cys Ala Ile
50 55 60

Gln Ile Thr His Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile
65 70 75 80

Thr Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Leu Leu Leu Lys
85 90 95

Ser Gly Cys Leu Glu Val Val Leu Val Arg Met Cys Arg Ala Phe Asn
100 105 110

Pro Leu Asn Asn Thr Val Leu Phe Glu Gly Lys Tyr Gly Gly Met Gln
115 120 125

```
Met Phe Lys Ala Leu Gly Ser Asp Asp Leu Val Asn Glu Ala Phe Asp
    130                 135                 140

Phe Ala Lys Asn Leu Cys Ser Leu Gln Leu Thr Glu Glu Glu Ile Ala
145                 150                 155                 160

Leu Phe Ser Ser Ala Val Leu Ile Ser Pro Asp Arg Ala Trp Leu Ile
                165                 170                 175

Glu Pro Arg Lys Val Gln Lys Leu Gln Glu Lys Ile Tyr Phe Ala Leu
            180                 185                 190

Gln His Val Ile Gln Lys Asn His Leu Asp Asp Glu Thr Leu Ala Lys
        195                 200                 205

Leu Ile Ala Lys Ile Pro Thr Ile Thr Ala Val Cys Asn Leu His Gly
    210                 215                 220

Glu Lys Leu Gln Val Phe Lys Gln Ser His Pro Glu Ile Val Asn Thr
225                 230                 235                 240

Leu Phe Pro Pro Leu Tyr Lys Glu Leu Phe Asn Pro
                245                 250
```

<210> 34
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORγ

<400> 34

```
Thr Pro Glu Ala Pro Tyr Ala Ser Leu Thr Glu Ile Glu His Leu Val
  1               5                  10                  15

Gln Ser Val Cys Lys Ser Tyr Arg Glu Thr Cys Gln Leu Arg Leu Glu
            20                  25                  30

Asp Leu Leu Arg Gln Arg Ser Asn Ile Phe Ser Arg Glu Glu Val Thr
        35                  40                  45

Gly Tyr Gln Arg Lys Ser Met Trp Glu Met Trp Glu Arg Cys Ala His
    50                  55                  60

His Leu Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Leu
65                  70                  75                  80

Ser Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Val Leu Leu Lys
                85                  90                  95

Ala Gly Ala Met Glu Val Val Leu Val Arg Met Cys Arg Ala Tyr Asn
            100                 105                 110

Ala Asp Asn Arg Thr Val Phe Phe Glu Gly Lys Tyr Gly Gly Met Glu
        115                 120                 125
```

Leu Phe Arg Ala Leu Gly Cys Ser Glu Leu Ile Ser Ser Ile Phe Asp
130 135 140

Phe Ser His Ser Leu Ser Ala Leu His Phe Ser Glu Asp Glu Ile Ala
145 150 155 160

Leu Tyr Thr Ala Leu Val Leu Ile Asn Ala His Arg Pro Gly Leu Gln
165 170 175

Glu Lys Arg Lys Val Glu Gln Leu Gln Tyr Asn Leu Glu Leu Ala Phe
180 185 190

His His His Leu Cys Lys Thr His Arg Gln Ser Ile Leu Ala Lys Leu
195 200 205

Pro Pro Lys Gly Lys Leu Arg Ser Leu Cys Ser Gln His Val Glu Arg
210 215 220

Leu Gln Ile Phe Gln His Leu His Pro Ile Val Val Gln Ala Ala Phe
225 230 235 240

Pro Pro Leu Tyr Lys Glu Leu Phe Ser Thr
245

<210> 35
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORγ

<400> 35
Ala Pro Glu Val Pro Tyr Ala Ser Leu Thr Asp Ile Glu Tyr Leu Val
1 5 10 15

Gln Asn Val Cys Lys Ser Phe Arg Glu Thr Cys Gln Leu Arg Leu Glu
20 25 30

Asp Leu Leu Arg Gln Arg Thr Asn Leu Phe Ser Arg Glu Glu Val Thr
35 40 45

Ser Tyr Gln Arg Lys Ser Met Trp Glu Met Trp Glu Arg Cys Ala His
50 55 60

His Leu Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Leu
65 70 75 80

Ser Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Ile Leu Leu Thr
85 90 95

Ala Gly Ala Met Glu Val Val Leu Val Arg Met Cys Arg Ala Tyr Asn
100 105 110

Ala Asn Asn His Thr Val Phe Phe Glu Gly Lys Tyr Gly Gly Val Glu
115 120 125

Leu Phe Arg Ala Leu Gly Cys Ser Glu Leu Ile Ser Ser Ile Phe Asp
130 135 140

```
Phe Ser His Phe Leu Ser Ala Leu Cys Phe Ser Glu Asp Glu Ile Ala
145                 150                 155                 160

Leu Tyr Thr Ala Leu Val Leu Ile Asn Ala Asn Arg Pro Gly Leu Gln
                165                 170                 175

Glu Lys Arg Arg Val Glu His Leu Gln Tyr Asn Leu Glu Leu Ala Phe
            180                 185                 190

His His His Leu Cys Lys Thr His Arg Gln Gly Leu Leu Ala Lys Leu
        195                 200                 205

Pro Pro Lys Gly Lys Leu Arg Ser Leu Cys Ser Gln His Val Glu Lys
    210                 215                 220

Leu Gln Ile Phe Gln His Leu His Pro Ile Val Val Gln Ala Ala Phe
225                 230                 235                 240

Pro Pro Leu Tyr Lys Glu Leu Phe Ser Thr
                245
```

<210> 36
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of human RORα

<400> 36

```
Gly Glu Thr Ser Pro Thr Val Ser Met Ala Glu Leu Glu His Leu Ala
  1               5                  10                  15

Gln Asn Ile Ser Lys Ser His Leu Glu Thr Cys Gln Tyr Leu Arg Glu
            20                  25                  30

Glu Leu Gln Gln Ile Thr Trp Gln Thr Phe Leu Gln Glu Glu Ile Glu
        35                  40                  45

Asn Tyr Gln Asn Lys Gln Arg Glu Val Met Trp Gln Leu Cys Ala Ile
    50                  55                  60

Lys Ile Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile
65                  70                  75                  80

Asp Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Val Leu Leu Lys
                85                  90                  95

Ala Gly Ser Leu Glu Val Val Phe Ile Arg Met Cys Arg Ala Phe Asp
            100                 105                 110

Ser Gln Asn Asn Thr Val Tyr Phe Asp Gly Lys Tyr Ala Ser Pro Asp
        115                 120                 125

Val Phe Lys Ser Leu Gly Cys Glu Asp Phe Ile Ser Phe Val Phe Glu
    130                 135                 140
```

```
Phe Gly Lys Ser Leu Cys Ser Met His Leu Thr Glu Asp Glu Ile Ala
145                 150                 155                 160

Leu Phe Ser Ala Phe Val Leu Met Ser Ala Asp Arg Ser Trp Leu Gln
                165                 170                 175

Glu Lys Val Lys Ile Glu Lys Leu Gln Gln Lys Ile Gln Leu Ala Leu
            180                 185                 190

Gln His Val Leu Gln Lys Asn His Arg Glu Asp Gly Ile Leu Thr Lys
        195                 200                 205

Leu Ile Cys Lys Val Ser Thr Leu Arg Ala Leu Cys Gly Arg His Thr
    210                 215                 220

Glu Lys Leu Met Ala Phe Lys Ala Ile Tyr Pro Asp Ile Val Arg Leu
225                 230                 235                 240

His Phe Pro Pro Leu Tyr Lys Glu Leu Phe Thr Ser
                245                 250
```

<210> 37
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fragment of murine RORα

<400> 37

```
Gly Glu Thr Ser Pro Thr Val Ser Met Ala Glu Leu Glu His Leu Ala
  1               5                  10                  15

Gln Asn Ile Ser Lys Ser His Leu Glu Thr Cys Gln Tyr Leu Arg Glu
            20                  25                  30

Glu Leu Gln Gln Ile Thr Trp Gln Thr Phe Leu Gln Glu Glu Ile Glu
        35                  40                  45

Asn Tyr Gln Asn Lys Gln Arg Glu Val Met Trp Gln Leu Cys Ala Ile
    50                  55                  60

Lys Ile Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile
65                  70                  75                  80

Asp Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Val Leu Leu Lys
                85                  90                  95

Ala Gly Ser Leu Glu Val Val Phe Ile Arg Met Cys Arg Ala Phe Asp
            100                 105                 110

Ser Gln Asn Asn Thr Val Tyr Phe Asp Gly Lys Tyr Ala Ser Pro Asp
        115                 120                 125

Val Phe Lys Ser Leu Gly Cys Glu Asp Phe Ile Ser Phe Val Phe Glu
    130                 135                 140

Phe Gly Lys Ser Leu Cys Ser Met His Leu Thr Glu Asp Glu Ile Ala
145                 150                 155                 160
```

```
Leu Phe Ser Ala Phe Val Leu Met Ser Ala Asp Arg Ser Trp Leu Gln
                165                 170                 175

Glu Lys Val Lys Ile Glu Lys Leu Gln Gln Lys Ile Gln Leu Ala Leu
            180                 185                 190

Gln His Val Leu Gln Lys Asn His Arg Glu Asp Gly Ile Leu Thr Lys
        195                 200                 205

Leu Ile Cys Lys Val Ser Thr Leu Arg Ala Leu Cys Gly Arg His Thr
    210                 215                 220

Glu Lys Leu Met Ala Phe Lys Ala Ile Tyr Pro Asp Ile Val Arg Leu
225                 230                 235                 240

His Phe Pro Pro Leu Tyr Lys Glu Leu Phe Thr Ser
                245                 250
```

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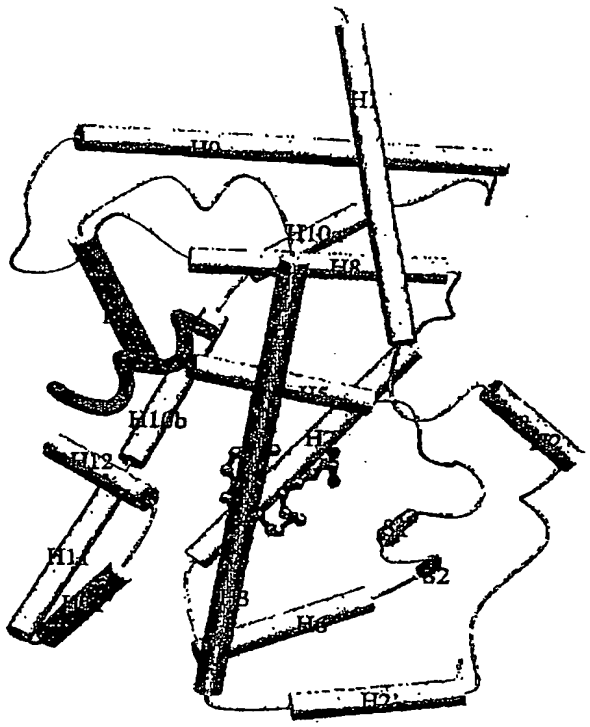
(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **MORAS, Dino** [FR/FR]; 38, rue de Pfulgriesheim, F-67450 Lampertheim (FR). **RENAUD, Jean-Paul** [FR/FR]; 15, rue NeuveEglise, F-67540 Ostwald (FR). **STEHLIN, Catherine** [FR/FR]; 31, rue Bautain, F-67000 Strasbourg (FR). **WURTZ, Jean-Marie** [FR/FR]; 7, rue des Saules, F-67404 Drusenheim (FR). **SCHUELE, Roland** [DE/DE]; Gauchmattenweg 7, 79367 Weisweil (DE). **GREINER, Erich, Friedrich** [DE/DE]; Brueckenstrasse 34, 69120 Heidelberg (DE).

(74) Agents: **GROSSET-FOURNIER, Chantal** et al.; Grosset-Fournier & Demachy S.A.R.L., 20, rue de Maubeuge, F-75009 Paris (FR).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,

[Continued on next page]

(54) Title: FRAGMENTS OF THE RETINOIC ACID-RELATED ORPHAN RECEPTOR (ROR) COMPRISING THE LIG AND BINDING DOMAIN (LBD), CRYSTAL STRUCTURE OF THE LBD OF ROR-BETA AND THEIR APPLICATIONS



(57) Abstract: The invention relates to polypeptides derived from the retinoic acid-related orphan receptor (ROR) in mammals, characterized in that they are delimited in their N-terminal extremity by an amino-acid located between positions 1 to 209, and in their C-terminal extremity by an amino-acid located between positions 450 to 452 of the rat RORß, α, or γ, or by an amino-acid located at corresponding positions in nuclear receptor ROR of other subtypes than α, β and γ, and/or of the other mammals. The invention also relates to the use of these polypeptides, or of the molecular complexes or the crystals containing them, for carrying out: -a process for the screening of a ROR-LBD ligand which is an agonist, or an antagonist of said receptor, - or a process for the analysis of the tridimensional structure of the complexes formed with said polypeptides, molecular complexes or crystals and a particular compound.

WO 03/000732 A3

SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) **Designated States** *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 02/05024

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C07K14/705 C12N15/33 G06F19/00 G01N33/50 //G06F159:00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K C12N G06F G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
BIOSIS, EPO-Internal, MEDLINE, WPI Data, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GREINER ERICH F ET AL: "Functional analysis of retinoid Z receptor beta, a brain-specific nuclear orphan receptor." PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 93, no. 19, 1996, pages 10105-10110, XP002194193 1996 ISSN: 0027-8424 the whole document page 10106, column 1, paragraph 3; figures 1,2 --- -/--	6,7,9-13

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
29 November 2002	16/12/2002

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax (+31-70) 340-3016	Petri, B

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	GREINER ERICH F ET AL: "Differential ligand-dependent protein-protein interactions between nuclear receptors and a neuronal-specific cofactor." PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 97, no. 13, 30 June 2000 (2000-06-30), pages 7160-7165, XP002194194 June 30, 2000 ISSN: 0027-8424 the whole document figure 2 ---	6,7,9-13
X	DATABASE EMBL 'Online! retrieved from EBI Database accession no. P35398; P51448; Q92753; P45446; P51449; P51450 XP002221987	6,7,9-13
Y	h/mROR-alpha; h/rROR-beta; h/mROR-gamma 1.6.1994; 1.10.1996; 1.11.1997; 1.11.1995; 1.10.1996; 1.10.1996; annotated LBD the whole document ---	14-17,21
X	WO 99 50660 A (RASPE ERIC ;BONHOMME YVES (FR); MERCK PATENT GMBH (US)) 7 October 1999 (1999-10-07) claims 1-17 the whole document ---	6,7, 9-13, 18-20
X	WO 00 24757 A (TULARIK INC) 4 May 2000 (2000-05-04) claims 25-43; figures 1,2 the whole document ---	6,7, 9-13, 18-20
X	WO 01 26737 A (NOVARTIS ERFIND VERWALT GMBH ;KNEISSEL MICHAELA (CH); NOVARTIS AG) 19 April 2001 (2001-04-19) claims 3-5 the whole document ---	6,7, 9-13, 18-20
Y	GILLILAND G L ET AL: "Crystallization of biological macromolecules for X-ray diffraction studies" CURRENT OPINION IN STRUCTURAL BIOLOGY, CURRENT BIOLOGY LTD., LONDON, GB, vol. 6, no. 5, October 1996 (1996-10), pages 595-603, XP002128062 ISSN: 0959-440X the whole document ---	14-17,21

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 02/05024

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ABOLA ENRIQUE ET AL: "Automation of X-ray crystallography." NATURE STRUCTURAL BIOLOGY, vol. 7, no. Supplement, November 2000 (2000-11), pages 973-977, XP001062873 ISSN: 1072-8368 the whole document	14-17,21
Y	BOURGUET WILLIAM ET AL: "Crystal structure of a heterodimeric complex of RAR and RXR ligand-binding domains." MOLECULAR CELL, vol. 5, no. 2, February 2000 (2000-02), pages 289-298, XP002194192 ISSN: 1097-2765 page 296, column 2, paragraph 3 the whole document	14-17,21
A	NOLTE R T ET AL: "LIGAND BINDING AND CO-ACTIVATOR ASSEMBLY OF THE PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR-GAMMA" NATURE, MACMILLAN JOURNALS LTD. LONDON, GB, vol. 395, 10 September 1998 (1998-09-10), pages 137-143, XP002906503 ISSN: 0028-0836 Discloses PDB:2PRG; identical topology (RMSD: 1.8A) with PDB:1K4W figure 1; table 2	8,20,21
P,X	STEHLIN CATHERINE ET AL: "X-ray structure of the orphan nuclear receptor RORbeta ligand-binding domain in the active conformation." EMBO (EUROPEAN MOLECULAR BIOLOGY ORGANIZATION) JOURNAL, vol. 20, no. 21, 1 November 2001 (2001-11-01), pages 5822-5831, XP002221986 ISSN: 0261-4189 the whole document	6-21

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 02/05024

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-5
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-5

Present claims 1-5 relate to a population of vaguely defined possible polypeptides.

The claims contain so many options that a lack of clarity and/or conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible.

The term "derived = deriveable" leaves the structural properties of the claimed polypeptides open to speculation. In its extreme interpretation any structural limitation is abolished.

The definition of N- and/or C-terminally truncated ROR-variants by reference to positions as represented on Fig. 3 is unclear and confusing: First of all, Fig. 3 does not contain all positions as claimed (e.g. positions 1-199 are missing). Furthermore, Fig. 3 depicts only partial h/mROR alpha-gamma molecules, leaving it open to speculation as to which residues of non-aligned molecules would correspond to the claimed boundaries.

Orphan receptors are receptors for which no ligands are known. Hence the functional definition of claim 3 does not impose any further limitation and is to be considered as a mere desireable property.

Reference to positions 459, 454, 458 in claim 4 is a contradiction in terms to claim 1, further obscuring the subject-matter for which protection is sought. Furthermore not all the claimed molecules have the claimed non-conserved cysteine residues.

In summary claims 1-5 contain so many obscurities, open terms and contradiction in terms, which render it difficult, if not impossible, to determine the matter for which protection is sought. As a consequence, the present application fails to comply with the clarity and conciseness requirements of Article 6 PCT (see also Rule 6.1(a) PCT) to such an extent that a meaningful search for claims 1-5 is impossible. Consequently, the search has been carried out for those parts of the application which do appear to be clear and concise, namely the subject-matter relating to Seq.Id.Nos. 2-37, of claim 6.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Int ɔnal Application No
PCT/EP 02/05024

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